us-09-987-701-2.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model protein õ

9, 2004, 16:39:47 ; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec August Run on:

US-09-987-701-2 Title: Perfect score:

514

1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries A Geneseq 29Jan04:\* geneseqp1980s:\*

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* 2: geneseqp1990s:\* 3: geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* South Works

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Aab95225 Human pro	0 Human		0	_	Abg21351 Novel hum	Abb60376 Drosophil		Novel	0	321	Abb59486 Drosophil	Aay79678 Drosophil	_		ø	Aab92844 Human pro	6 Novel	Abr53774 Protein s	Aar85881 WD-40 dom	œ	119	040	Aab68282 Amino aci	Aag48120 Arabidops
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### ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                      Human protein sequence SEQ ID NO:17352.
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             AAB95225 standard; protein; 514
                                                                                                                                            27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-002183767.
99-JUN-2000; 2000JP-00241899.
                                                                                                                       28-JUL-2000; 2000EP-00116126.
                                                                                                                                      99JP-00248036.
                                       (first entry)
                                                                                                                                                                             (HELI-) HELIX RES INST
                                                                                                                                      29-JUL-1999;
                                                                                 Homo sapiens.
                                                                                             EP1074617-A2.
                                        26-JUN-2001
                                                                                                          07-FEB-2001.
                           AAB95225;
RESULT 1
AAB95225
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Yamamoto J; T; Saito K, , Otsuki Hayashi K, S A, Nagai K, Isogai T, Nishikawa T, Sugiyama T, Wakamatsu Ota T, Is Ishii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 'end sequence, where the oligonucleotide comprises at least is nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AMP01366 to AAM13628 and AAM13631 to AAM13642 represent human amino acid sequences; and AAM13629 to AAM13621 represent oligonucleotides, all of which are used in the exemplification of the
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99.4%; Pred. No. 1.1e-242;
ive 2; Mismatches 1;
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Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53

Example 2; Page 458-459; 678pp; English.

pathway in Drosophila.

Funke RP;

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ij Ä

Francis-Lang

Belvin M,

Friedman L, Plowman GD,

WPI; 2003-156859/15. N-PSDB; ACD13365.

EXEL-) EXELIXIS INC

03-JUN-2002; 2002WO-US017382. 05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P.

WO200299122-Al. Homo sapiens.

12-DEC-2002

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                                                                                                                              The invention relates to identifying (M1) a candidate p53 pathway
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                                                                                                                                                                                                                                                                                          Length 514;
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                                                                                                                                                                                                                                                                                    99.3%; Score 2708; DB 6;
Local Similarity 99.4%; Pred. No. 2.2e-242;
tes 511; Conservative 1; Mismarch.
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Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

Human p53 modifying protein, SEQ ID 150.

13-AUG-2003 (first entry)

ABO07190 standard; protein; 514 AA

RESULT

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The present invention describes a predictor set comprising a plurality of polynucleocides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of determining whether the cells comprising obtaining a sample of cells, correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels
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                                                                                                                                                                                      GNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF 420
                                                                                ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKQNFILSAGVDKTTIIWDAHTGEA
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                         SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                            ATGSYDGFARIWTXDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADD14051 standard; protein; 577
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correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polymuclectides and polypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polymuclectides or polypeptides, and selecting polymuclectides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the polymuclectides have cytostatic activities, and can be used in gene therapy. The polymuclectides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining dentity to profile which aid in treating diseases and disorders (e.g. genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present content of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ATAATTTSAGVSHQNPSKNREATVNGEENRAHSV-NNHAKPMEIDGEVEIPSSKATVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 KTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 HINEVNAIKWDPSGMLLASCSDDMTLKIWSMKQEVCIHDLQAHNKEIYTIKWSPTGPATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 NPNSNIMLASASFDSTVRLWDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 KTTIIWDAHTGEAKQQFPFHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 HTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPNANLMLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ------ASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian; breast; cancer; tumour;
tumour; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                       89.4%; Score 2437; DB 7; Length 577; 86.0%; Pred. No. 4e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 IWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 IWNTQSCNLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK
                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              453; Conservative 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP41760 standard; protein; 542
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ovarian cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian antigen HNOKM38,
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     Sequence 577 AA;
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The invention relates to 2175 novel human ovarian antigens (ABB41054-ABB43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polybrucleorides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen corrections and host cells comprising human ovarian antigen of ovarian antigens and the use of ovarian antigens and proposing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tunnous of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired condeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaenia), cardiovascular disorders and urinary system disorders, neurological disorders, gastrointestinal disorders and urinary system disorders, ovarian antigen polypeptides and of confine evarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies indentification of individuals and in forensic analysis, and the confine sequence data for this patent did electronic format directly from MIPO sequence data for this patent did electronic forme part of the printed sequence data for this patent did electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorthoea; endocrine disorder; infection; infinamatory condition; immune disorder; blood disorder; acardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibofammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 2892; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2001; 2001WO-US018569
                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2000; 2000US-0209467P.
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Best Local Similarity 85.4'
Matches 434; Conservative
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                                                                                                                                                                                                                                                                            WO200200677-A1.
                                                                                                                                                                                                                              Homo sapiens.
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CSDDMTLKIWSMKQEVCIHDLQAHNKEIYIIKWSPTGPATSNPNSNIMLASASFDSTVRL 454
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                              GFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQGHTNEVNAIKWDPSGWLLAS
                                                                                                                                                                                                                                                       GFARIWTEDGNLASTLGQHKGPIFALKWNRKGNYILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 REATVNGEENRAHSV-NWHAKFWEIDGEVEIPSSKATVLRGHESEVFICAWNPVSDLLAS
                                                                                                                                                                                                                            GSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLLATGSYD
                                                                                                         GENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
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2000US-0230514P.
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05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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Length 542;

28; Indels

85.8%; Score 2340; DB 5; 85.4%; Pred. No. 3.8e-208; ive 32; Mismatches 28;

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The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a treatment (MDDT) polypeptide (I) selected from a polypeptide having a treatment (MDDT) polypeptide (GMPP131.ABP13484) given in the sequence selected from 254 sequences (AMPP12131.ABP13484) given in the specification, a naturally occurring polypeptide comprising a sequence (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polydonal or monoclonal antibody by hyptidems technology.

Nucleic acids (II) (ABD72449-ABD7200) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target of polymucleotides and antibody by hyptidems technology.

Nucleic acids (II) (ABD72449-ABD7200) encoding (I) are useful for certification a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a sample. A composition comprising (I), an agonist or antagonist is useful for treating a disease or condition associated with decreased or increased expression of functional MDDT. (I) or associated with decreased or increased expression of functional MDDT. Or (II) are useful for diagnosing, treating or preventing disorders are selected from a cell proliferative disorder and an associated with aberrant expression of MDDT, where the disorders are cirrhosis, hepatitis, poriasis, and cancer and an autoimmune/inflammatory disorder such as AIDS, Addison's disease, allowable of a tissue or cell cirrhosis, hepatitis. (II) are useful for creating drockin humanised animals or transgenic animals to model human disease; in somatic or type, for detecting differences in the chromosomal location due to commune. The expension or inversion among normal, carrier or affected individuals and annease.
                                                                                                                                                                                                                                                                                                          Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS;
Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE;
Dahl CR, Momiyama MG, Bradley DL, Rohatqi SD, Harris B;
Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V;
Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g. AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Page 578; 618pp; English.
06-SEP-2000; 2000US-023059BP.
06-SEP-2000; 2000US-023059BP.
06-SEP-2000; 2000US-023061DP.
06-SEP-2000; 2000US-023086EP.
06-SEP-2000; 2000US-023098BP.
07-SEP-2000; 2000US-023198P.
07-SEP-2000; 2000US-0231163P.
07-SEP-2000; 2000US-0231163P.
                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.5
Matches 389, Conservative
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                                                                                                                                                                                                                      301 KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                             SDILLASGSGDSTARIWNLSENSTSGSTQLVLKHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                      245 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAMNPV
                                 OGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPV
                                                                       SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                       GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 395
                                                                                                                                                                                                                                                                                                 GNILLASCSDDMTLKIWSMKQDNCVHDLQQHN 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #21342.
                                                                                                                                                                                                                                                                                                                                                                                                                              ABG21351 standard; protein; 584
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23-AUG-2000; 2000US-00649167,
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1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV 60 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV 64

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7920; 21pp + Sequence Listing; English
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                                                       2000US-0191637P.
2000US-00614150.
                              23-MAR-2001; 2001WO-US009231.
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                                                                                                   (PEKE ) PE CORP NY
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                                                         23-MAR-2000;
11-JUL-2000;
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   27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                           --- AAASQQGSA 124
                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                           70.0%; Score 1907.5; DB 4;
llarity 65.1%; Pred. No. 6.7e-168;
Conservative 34; Mismatches 36; I
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Best Local Similarity
Matches 371; Conserv
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                                                                  EVEWSVGEDGEV - - ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN
                                                                                                                                                                              119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDOSASEVDSSGNAANNAGGTYAGNNG
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Length 700;
                           Indels
  DB 4;
  69.9%; Score 1904.5; DB 4 54.8%; Pred. No. 1.7e-167; ive 51; Mismatches 75;
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    Query Match 69.9
Best Local Similarity 54.8
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developmental biology; cell signalling; insecticide;

WO200171042-A2

pharmaceutical

Drosophila melanogaster polypeptide SEQ ID NO 7920

entry)

(first

ABB60376 standard; protein; 700

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1 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL

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LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
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NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders, arthritis, inflammation.
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                                                                                                                                                       TGQLVHSYKGTGGIFEVCWNSKGTKVGASASDGSVFVLDLRK 699
                                                                                                                                     TGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                        AA004385 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 18277.
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18-MAY-2000; 2000US-00577409.
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Matches 206; Conservative
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N-PSDB; AAI84316.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abgooulo-Abg30377 represent novel human diagnostic manno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                         61 KWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIH 120
                                                                                   333 VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNK 392
                                                                                                                        121 VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNK 180
  KWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIH 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 51709; 103pp; English.
                                                                                                                                                                  EIYTIKWSPTGPGTNNPNANLMLASAS 419
                                                                                                                                                                                            EIYTIKWSPTGPGTNNPNANLMLASAS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #21341.
                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                              ABG21350 standard; protein; 167
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                               entry)
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N-PSDB; AAS85537.
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272

213 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGPARIWTKDGNLASTLGQHKGPIFAL

Gaps

97;

Length Indels 49 20

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155 219 214 279 274 324

101

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384 394 444 444 481

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17-AUG-2001; 2001US-0313245P. 24-AUG-2001; 2001US-031475IP. 31-AUG-2001; 2001US-0316752P.

Sequence 535 AA

334

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50 ISIIQKGLQYVEABVSINEDG---TLFDGRPIBSLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                                                 .07 QAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 IFAGRISQDGQKYAVAFMDGQVNVYDLKKLNSKSRSLYGNRDGILNPLPIPLYASYQSSQ 504
                                                                                                                                                                                                                                                                                                                                  167 GHESEVFICAMNPVSD-LLASGSGDSTARIMNLSENSTSGSTQ-----LVLRHCIREGG
                                                                                                                                                                                                                                                                                                                                                            215 SSGKTINQVFCLAWSHDGNSIVTGVENGELELWNKTGALLNVLNFRAPIVSVKWNKDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILSAGVDKTTIIWDAHTGEAKQQFPF------HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 HISMDVENVTILWNVISGTVMQHPELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 CSTDMCIHVCKIGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 PGPKGAIFVYQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSQ
                                                                                                                                                                                                                                                                           385 HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 NCFYGHSQSIVSASWV------GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                     220 ODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGOHKGPIFALKWNKKGN
                                                                                   -----FTFGIKSHISQSNINGALVPPAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, intracellular signalling molecule; INTSIG; cell proliferative disorder; cancer; atherosclerosis; autoimmune disorder; inflammatory disorder; infection; neurological disorder; developmental disorder; endocrine disorder; cytostatic; antiarteriosclerotic, nootropic; neuroprotective; cerebroprotective; immunosuppressive; antiinflammatory; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human intracellular signalling molecule INTSIG-3, SEQ ID NO:3
                                                                                                           Query Match
18.3%; Score 499.5; DB 6;
Best Local Similarity 24.9%; Pred. No. 4.3e-37;
Matches. 142; Conservative 100; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 VYSVAFSPDGRYLASGSFDKCVHIW-----NTQTGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 DNDYIFDLSWNCAGNKISVAYSLQEGSVVAI 535
                                                                                   1 MSISSDEVNFLVYRYLQESGFSHSA-
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                                                                                                                                                                                                                                                          369
                                                                                                                                                                                                                                                                                  RIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSA 309
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                                                                                                                                                                                                     RIWTENGNLAITICQHKGPIFALKWNKKGNYVLSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                                          PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTGNLLASCSD
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                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 825; 17pp + Sequence Listing; English
                                                                                            Length 167;
                                                                                                                                                                                                                                                                                                                                             DMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLA
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multiprotein complex; eukaryote; drug target; diagnosis
                                                                                                                                   10;
                                                                                       ; Score 819; DB 4;
; Pred. No. 1.4e-67;
13; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i P, Krause R, K
Superti-Furga GD;
             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 535
                                                                                         30.0%;
86.2%;
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Marzioch M, Schultz JD,
                                                                                                                                     Matches 144; Conservative
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                                                                                                                  Similarity
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                                                      Sequence 167 AA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to 45 human intracellular signalling molecules (INTSIG), INTSIG-1 to INTSIG-45, and the cDNAs encoding them (ADA1319-ADA1408). The invention also encompasses expression constructs, host calls and transgenic organisms comprising an INTSIG nucleic acid sequence; the recombinant preparation of a INTSIG; an antibody against a INTSIG; eachods of detection of INTSIG proteins or nucleic acids; am micro-array containing INTSIG nucleic acids; methods of screening compounds for their ability to modulate INTSIG acitvity or expression; and pharmaceutical compositions comprising an INTSIG protein, an INTSIG antibody, an INTSIG aponist or INTSIG antagonist. The INTSIG proteins, mucleic acids or compositions comprising them are useful in diagnosing, treating or compositions comprising them are useful in diagnosing, treating or preventing a variety of disorders, including cell proliferative disorders (e.g., AIDS, allergies, anaemia, asthma, Dronchitis, gout, multiple sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus cervitemancosus; neurological disorders (e.g., epilepsy, stroke, alloredies disorders (e.g., epilepsy, stroke, Alzheimer's disease); viral, bacterial, comparation, or parkinson's disease); developmental disorders (e.g., achondroplastic dwarfism, cushing's disease, hypothyroidism or hydrocephalus); endocrine disorders (e.g., disorders of the hypothalamus or pituitary gland or disorders (e.g., disorders of the hypothalamus or pituitary gland or clabetes); reproductive disorders; or vesicle-trafficking disorders (e.g., represents an INTSIG protein of the invention.
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                                                                                                                                                                                   , Emerling BM;
Becha SD, Lee EA;
gan BM, Gietzen KJ;
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                                                                                                                                                                                                                                                                      Nguyen DB;
                                                                                                                                                                                                                                                                                                                                                                                           New human intracellular signaling molecules (INTSIG)), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDG
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                                                                                                                                                                                     Lu DAM, Swarnakar A, Tang YT, Griffin JA, Emerling BM.

IJ, Yao·MG, Ramkumar J, Richardson TW, Becha SD, Lee
A, Lehr-Mason PM, Baughn MR, Li JX, Duggan BM, Gietzz
Borowsky ML, Thangavelu K, Xu Y, Lee S;
VS, Sprague WW, Azimai Y, Hafalia AJA, Ding L, Nguye
CD, Luo W, Chawla NK, Marquis JP, Jackson JL, Tran I
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; Pred. No. 1.2e-25;
49; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 225-226; 367pp; English
31-AUG-2001; 2001US-0316847P.
14-SEP-2001; 2001US-0322188P.
28-SEP-2001; 2001US-0326390P.
12-OCT-2001; 2001US-0345468P.
19-OCT-2001; 2001US-0345468P.
12-APR-2002; 2002US-0372499P.
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                                                                                                                                                 (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                 Sprague WW,
Luo W, Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.7
Best Local Similarity 28.3
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                WPI; 2003-393436/37.
N-PSDB; ADA13366.
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Honchell CD,
                                                                                                                                                                                                                                                al PG, Bor
lliott VS,
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Warren BA,
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TGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASAS 419
                                                 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences. (ABL01840-ABL16175) and the encoded proteins (ABBS7077-ABR2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GHAEAVVSLNPSPDGAHLASGSGDTTVRLWDLNTETPHFTCTGHKOWVL--CVSWAPDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EGGQD-----VPSNKDVTSLDW-----NSEGTLLATGSYDGFAR
                                                 ---NPQGNHLLTGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 KNEBATPYLFFVGEDEIKKSLEDT-LDLASVDTENVIDIVYQPQAVFKVRPVTRCTSSMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIR----
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                                                                                                         469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
                                                                                                                                                           413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                      FDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 KNGENTAN----GEENGAHTIANNHTDMMEVDG----DVEIPPNKAVVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                 TGKLIATASADGTARIFSAATRKCIAKLEGHEGEISKISF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 5250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EN.
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                                                                                                                                                                                                                                                                                                 ABB59486 standard; protein; 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
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pharmaceutical
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modified Notch signalling activity in a variety of Notch-dependent signalling process in both Drosophila and Xenopus embryos. The Notchless protein has a novel highly conserved N-terminal domain followed by 9 MP40 repeats. Notchless, and nucleic acids encoding it, can be used in methods for the diagnosis and therapy of certain diseases, particularly cancer and neurodegenerative diseases (claimed). A Notchless mutant in a sensitised Notch genetic background is used in a claimed method for identifying compounds capable of modifying the levels of expression or activity of a Notch protein
                                                                                                                                                                                                                                                                                                                                                                                             276 KKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 GAG-LIYTSSKDRTVKANWRAADGILCRTFSGHA-----HWVNN---IALSTD---YVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 LGQDRPIK-TFQGH----TNEV----NAIKWDPTGNLLASCSDDMTLKIWSMKQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 TGPFHPVKDRSKSHLSLSTEELQESALKRYQAVCPDEVESLV-SCSDDNTLYLWRNNONK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 CVERMICHQNVVNDVXYSPDVK-----LIASASFDKSVRLWRASDGQYMATFRGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 VRLWDLNTETPHFTCTGHKQWVL--CVSWAPDGKRLASGCKAGSIIIWDPETGQQKGRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 VPSNKDVTSLDW-----NSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 EPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGAS
                                                                                                                                                                                                                                                                                                                                                              147 DMMEVDG----DVEIPPNKAVVLR------GHESEVFICAWNPVSDLLASGSGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EGGOD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                          Length 479;
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                          .Match 13.6%; Score 370; DB 3; L
Local Similarity 28.4%; Pred. No. 4e-25;
les 120; Conservative 55; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 ARIWNLSEN----STSGSTQLVLRHCIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                  Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
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                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of Notchless, a novel protein of Drosophila. Notchless was identified in a screen for dominant modifiers of a Notch mutant phenotype in the Drosophila wing. The mutant dominantly suppressed the wing notching phenotype of notchind mutations, and the Notchless protein was shown to bind to the cytoplasmic domain of Notch. Notchless
                                                                                                                                                                                                                                                                                                                                              476
                                                                                                                                                                                                                                                         416
                                                                                                                                                                                                                                                                                                                                                                      --TNEV-----NAIK 356
                                                                                                                                                                                                   ----HWVNN---IALSTD---YVLRTGPFHPVKDRSKSHLSLSTEELQESALKRYQAVC 334
                                                                                                                                                                                                                                                                                                    384
                                                                           IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has
         RLASGCKAGSIIIWDPETGQQKGRPLSGHKKHINCLAWEPYHRDPECRKLASASGDGDCR
                                                                                                                                                                                                                                                                                                 PDEVESLV-SCSDDNTLYLWRNNQNKCVERMTGHQNVVNDVKYSPDVK-----LIA
                                                                                                       WDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLA
                                                                                                                                                                                                                                                                                                                                              SASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "sequence deduced from nucleotide sequence additional Lys residue between Lys-67 and Ser-68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel notchless protein and nucleic acids encoding them useful treating and preventing cancer and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notchless; Nle gene, Notch, signalling, neurodegeneraticancer; diagnosis; cytostatic; neuroprotective; therapy
                                                                                                                                                                    PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIK-TFQGH-
                                                                                                                                                                                                                                                                                                                                                                                                                                     VHSYRG-TGGIFEVCWNAAGDKVGASASD 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQELPGHADEVFGVDWAPDGSRVASGGKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "encoded by CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27. .105
/note= "Nle domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY79678 standard; protein; 479 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Royet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila Notchless protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-IB001891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QDVA-----FDAQGK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLATGSYDGFARIW--TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------YC----VKTYTGHREWVRMVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNAN---LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 EVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAAQQG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in alucidating cell signalling and call-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     :||:|| :||:|| :|| :|| || ::|| || EELNQAIADYLGSNGYADSLETFRKEADLSTEVEKKFGGLLEKKWTSVIRLQKKVMELEA
                                                                                                                                                                                                                                                                                                                                                                                                                             123 SAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVIRGHESEVFICAMNPVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 WDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP-----TGPGTNN
                                                                                                                                                                                                                                                                                                                Gaps
                                                                            New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signaling and cell-
                                                                                                                                                                                                                                                                                         13.5%; Score 368; DB 4; Length 411; 22.7%; Pred. No. 4.8e-25; ive 76; Mismatches 151; Indels 148;
                                                                                                                        Disclosure; SEQ ID NO 13572; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 LMVSASEDATIRIWDFETGEYERSLKGHTDSV---
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                      EM.
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standard; protein; 485 AA

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                                                                                                 bone marrow transplantation; rheumatoid arthritis; lupus erythematosis; multiple sclerosis; encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis; thyroiditis; malignant disorder; asthma; lepramatosis; gastritis; skin tumour; adrenal tumour; lung tumour; wound healing; growth disorder; inflammatory disease; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide encoding TZap protein involved in T cell activation, useful for diagnosing and treating diseases involving T cell activation, for treating organ transplantation rejection, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QSNNTFASCS 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "unspecified residue encoded by
                                                                       cell activation; immune response; transplant
acid sequence of a human TZap gene cDNA clone.
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                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
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25-FEB-2000; 2000US-0185016P.
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446 YSVAFSPDGRYLASGSFDKCVHIW 469
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460 YAVDWSPDGQRVASGGKDKCLRIW 483
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289 WVNTMALSTDYALRTGAFEPAEASVNPQDLQGSLQELKERALSRYNLVRGQGPERLVSGS 348

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Search completed: August 9, 2004, 16:45:24 Job time: 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

August 9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec

US-09-987-701-2
2726
1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	homod	у рошо	homod	mus n		anabaena	Q8ytc2 anabaena sp	podospora				_					pos										P49846 drosophila	Ω			ပ္ပ	ä	Q23256 caenorhabdi
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	Score	2716	2437	2367	1304	502.5	479	463.5	460	445.5	388.5	366.5	365.5	365.5	348.5	348	346.5	345.5	344.5	340.5	339.5	339	334	329	321	319.5	317.5	310.5	309	308	307	304	300	294.5
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T2D4_SCHPO TU11_SCHPO	rzin Caesi GBBS HUMAN GBBS MOUSE TU12 SCHPO	FW1A_HUMAN LUG_ARATH PRP4_ARATH	GBB MAIZE TUPI YEAST PRP4_HUMAN
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# ALIGNMENTS

RESULT 1 TEBLA HUMAN ADD TO 28-FEB DD TO 28-FEB TEBLATION COC BURNAN RRY MEDLII RRY RRY RRY MEDLII RRY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, BC032708, AA432708.1, -
Genew, HGNC:11585, TBLIX.
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DOMAIN 4
                    [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
TISSUE=Lymph;
          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                 GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
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                                                                                                                                                                                                                                                     1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                           301 KOOFPFHSAPALDVDWOSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-07T-2001 (Rel. 40, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                  .
0
                                                                                                                                                                                               Length 514;
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                                                                                                                                                 -> K (IN REF. 2).
-> H (IN REF. 3).
-> Q (IN REF. 2).
0B556D2EE4BA796D CRC64;
                                                                                                                                                                                               99.6%; Score 2716; DB 1; 99.6%; Pred. No. 1.5e-188; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 AA.
         PROSITE; PS50896; LISH; 1.
PROSITE; PS00678; WD REPEARS 1; 4.
PROSITE; PS50082; WD REPEARS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                     LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 5.
WD 6.
WD 7.
WD 8.
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 SMART; SM00320; WD40; 8.
                                               WD repeat.
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Matches 512;
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060907;
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                                                                                                                                                                                                                                                                                                                                                                                                                    A Tables-1978 Pubbmed=12477932;

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A Lausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Lausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

A Latchento E.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

Batchento E., Warnsina K., Farmer A.A., Rubin G.M., Hong L.,

Batchento E., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Talan D.K., Muany D.M., Sodergren E.J., Lu X., Gibs R.A.,

A Talay D.K., Muany D.M., Garcia A.M., Gay L.J., Hulyk S.W.,

A Talay D.K., Muany D.M., Schergen E.J., Lu X., Gibs R.A.,

A Hilalon D.K., Muany D.W., Greenen B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Greenen B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Greenen B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length

R. Froc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

1- SIMILARITY: Contains 8 WD repeats.
                                              Grandi A.
MEDLINE=99264241; PubMed=10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.;
"X-linked late-onset sensorineural deafness caused by a deletion involving OA1 and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616(1999).
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SMART, SM00320; WD40; 7.
PROSITE; PS50896; LISH; 1.
PROSITE; PS50078; WD. REPEATS 1; 4.
PROSITE; PS5002; WD. REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS 2; 6.
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                                                                                                                                                                                                                                               1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                       EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAA---
                                                                                                                                                                                   -----ASQQGSAKNGENTANGBENGAHTIANNHTDMMEVDGDVEIPPNKAVVIRG
                                                                                                                                                                                                                                  HESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKD
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                                                                        Gaps
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O9BQ97,
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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Wilson R.K., Waterston R.H., Page D.C.;
"The DNA sequence of the human Y chromosome.";
Submitted (BCC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 LisH domain.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                      14;
                                                Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
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  WD 8.
POLY-ALA.
98922F88EC42F6E9 CRC64;
                                                                     27;
                                            89.4%; Score 2437; DB 1;
86.0%; Pred. No. 2.1e-168;
ive 33; Mismatches 27;
 525 WD
124 POI
57048 MW;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
                                            Query Match
Best Local Similarity 86.03
Matches 453; Conservative
 493
108
526 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 86.8%; Score 2367; DB 1; Best Local Similarity 84.5%; Pred. No. 2.4e-163; Matches 442; Conservative 35; Mismatches 34;
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                            EMBL, AF332220; AAK13472.1; EMBL, AF332221; AAK13473.1; EMBL, AF332222; AAK13474.1; Genew, HOVC.18502; AAK13474.1; Genew, HOVC.18502; TBLY.

InterPro; IPRO06594; LisH.

InterPro; IPRO01680; WD40.

PEMINTS; PR00320; GPROTEINBRPT.

PRODCH; PR00018; WD40; 8

PRINTS; PR00667; LisH; 1.

SWART; SW00667; LisH; 1.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50896; WD REPEATS_2; 6.

PROSITE; PS5082; WD REPEATS_2; 6.

PROSITE; PS5082; WD REPEATS_2; 6.
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522 AA;
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TBLX MOUSE
ID TBLX MOUSE
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                                                                                                                                                                                                                                                                                                                                                           Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston P., Hunter G., Kimberly C., Rhodes M., Submitted (SEP-1999) to the EMBL/Genbank/DDBJ databases.

-i. SIMILARITY: Contains at least 5 WD repeats.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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115 WD 2.
198 WD 3.
249 WD 4.
291 WD 5.
313
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                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
17-ATABGAUCIN beta-like 1X protein (Fragment)
TBLIX OR TBLI
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InterPro; IPR001680; WD40.
FEAM, PF00400, WD40.
FRIMTS, PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
SWART; SW00320; WD40; 2.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50029; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_2; 4.
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SIF2\_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. . .; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jens F. 15:2991-3004 (2001).

-! FUNCTION: Antagonizes telomeric silencing in yeast. May recruit genes Dev. 15:2991-3004 (2001).

-! FUNCTION: Antagonizes telomeric silencing in yeast. May recruit SIR4 to nontelomeric sites or repression.

-! SUBURT: Interacts with SIR4 amino-terminal domain. Interacts with a complex composed of SIN3 and RPD3. Identified in the Set3C complex with HOS2, HST1, SNN1, CPR1, HOS4/YIL112W and SET3.

-! SUBCELLULAR LOCATION: Nuclear.

-! SIMILARITY: Contains 1 Lish domain.

-! SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                         Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II."; Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21567937; PubMed=11711434; MEDLINE=21567937; PubMed=11711434; MEDLINE=21567937; PubMed=11711434; Milm M., Rigaut G., Seraphin B., Aasland R., Stewart A.F.; Wilm M., Rigaut G., Seraphin B., Aasland R., Stewart A.F.; The S. cerevisiae SET3 complex includes two histone deacetylases, Hosz and Hstl, and is a meiotic-specific repressor of the sporulation gene program."
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R EMBL; Z35972; CAA85058.1; -.

R EMBL; Z35972; CAA85058.1; -.

R GERMONINE; 138646; -.

SGD; S0000307; SIF2.

R GO; GO:000118; C:histone deacetylase complex; IPI.

R GO; GO:0017136; F:NAD-independent histone deacetylase activity; IDA.

R GO; GO:0017129; F:NAD-independent histone deacetylase activity; IDA.

R GO; GO:000548; P:NAD-independent histone deacetylase activity; IDA.

R GO; GO:000129; P:NAD-independent histone deacetylase activity; IDA.

R GO; GO:000125; P:negative regulation of meiosis; IPI.

R GO; GO:000125; P:negative regulation of transcription from P. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cockell M., Renauld H., Watt P., Gasser S.M.; "Sit2p interacts with Sir4p amino-terminal domain and antagonizes telomeric silencing in yeast."; Curr. Biol. 8:787-790(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DENTIFICATION IN A COMPLEX WITH HOS2; HST1; SNT1; CPR1; YIL112W
                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity;
                                    (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 42, Last annotation update)
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PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
                                                                                                       SIR4-interacting protein SIF2.
SIF2 OR EMB1 OR YBR103W OR YBR0832.
                                                                                                                                                                                                                                                                                                     MEDLINE=95208357; PubMed=7900426;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98315485; PubMed=9651685;
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GO; GO:0000534; C:nucleus; I
GO; GO:0017136; F:NAD-indepen
GO; GO:000534; F:NAD-indepen
GO; GO:0006348; P:Chromatin
GO; GO:0016575; P:nbgatin
GO; GO:0016575; P:nbgative rr
InterPro; IPR006594; Lish:
InterPro; IPR00180; WD40.
FroDom; PD000018; WB40; I.
SWART; SW00667; Lish: I.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                STRAIN=S288C
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Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 SSGKTTNOVTCLAWSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWNKDGT 274
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                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                       DB 1; Length 535;
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25DD19AB2BFB4B07 CRC64;
                                                                                                                                                                                                                                                                                                                                    18.4%; Score 502.5; DB 1; Length llarity 24.9%; Pred. No. 8.2e-29; Conservative 100; Mismatches 232; Indels
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Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
NCBI_TaxID=103690;
1D_REPEATS 2; 4.
ND_REPEATS_REGION; 1.
Chromatin regulator; Nuclear protein.
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ALR3466.
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MD 3.
MD 4.
MD 5.
MD 6.
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3 208
3 208
5 298
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8 396
5 59145 MV;
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396
335 AA;
                                                  WD repeat;
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SEQUENCE FROM N.A.
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28-FEB-2003
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Matches 142;
  PROSITE;
PROSITE;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T., Kibhida Y., Kohara M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res 8.205-213 (2001).
-! SIMILARITY: Contains 1 pentapeptide repeat domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A INTEGERIO; ACCOUNTS,
R FERM; PROUBLO; MS-0, 15.
R PRINTS; PROUBLO; WS-0, 15.
R PRODOM; PROCOTEINBRPT.
R PROSITE; PSCO078; WD_REPEATS 1; 11.
R PROSITE; PSCO078; WD_REPEATS 2, 15.
R PROSITE; PSCO094; WD_REPEATS 2, 15.
R PROSITE; PSCO094; WD_REPEATS 2, 15.
R PROSITE; PSCO094; WD_REPEATS REGION; 1.
R PROSITE; PSCO097; WD_RCHT; UNKNOWN 1.
R PROMAIN 823 862 PENTAPEPTIDE.
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1366 1405 WD 14.
1408 1447 WD 15.
1450 1491 WD 16.
1526 AA; 170376 MW; D5DF272509B4A738 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003593; BAB75165.1; -.
BIR; AC2293; AC239.
INTERPRO; IPR00711; NACHT_NTPASE.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                           1100 -----LRGHSNRYYSAIFSPNGEIIATCSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1153 AFSPDGK-----ILASASHDQTVRIWDVNTGKCHHICIGHTHLVSSVAFSPDGEVV 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTOLVLRHCIREGGODVPS
                                                                                                                                                                                                                                                                                                                      225 NKDVTSLDW-----NSEGTLLAIGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                     278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
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MEDLINE=96009891; PubMed=7557402;
Saupe S., Turcq B., Begueret J.;
A gene responsible for vegetative incompatibility in the fungus
Pedospora anserina encodes a protein with a GTP-binding motif and G
beta homologous domain.";
                                                                                   Length 1258;
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Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
                                                                                                                                                                                                                                                              974 LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH-
                                                                                                                                           Indels
1186 1227 WD 15.
1258 AA; 139513 MW; 45DF03B91170C451
                                                                                   17.0%; Score 463.5; DB 1;
Similarity 31.8%; Pred. No. 1.7e-25;
03; Conservative 44; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-ULL-1998 (Rel. 36, Created)
15-ULL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetatible incompatibility protein HET-E-1.
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PIR; T18521; T1852.
InterPro; IPR007111; NACHT_NTPASE.
InterPro; IPR001680; WD40.
Pfan; PP05729; NACHT; 1.
Pfan; PF00400; WD40; 10.
                                                                                                                                              Matches 103; Conservative
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                                                                                                                                                    1450
   482
                                                                                                                            TVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILIPE-2155-2595; PubMed=11759840; Kuritz T., Sasamoto S.,
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Makazawa M., Yanada M.,
Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
--- SIMILARITY: Contains 1 NB-ARC domain.
--- SIMILARITY: Contains 15 WD repeats.
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PROSITE; PS00678; WD REPRATS 1; 9.

PROSITE; PS50082; WD REPRATS 2; 14.

PROSITE; PS50294; WD REPRATS REGION; 1.

Hypothetical protein; Repeat; WD repeat; Complete proteome. REPRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                 1451 HINSVRSVAFSSDGLILASGSDDETIKLWDVK 1482
                                                                                                                                                                                                               513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1258 AA
                                                                                                                                                                                                               483 -TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical WD-repeat protein alr2800.
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InterPro; IPRO02182; NB-ARC.
InterPro; IPRO01680; W040.
Pfam; PF00400; ND40; 1.
PRIMS; PRO0320; GPROTEINBRPT.
PRIODOM; PD000018; WD40; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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975
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1101
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NCBI_TaxID=103690;
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28-FEB-2003
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Q8YTC2;
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482 GTGGIFEVCWNAAGDKVGASASD 504
 MEDLINE=21595285; PubMed=11759840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAASGICTOTLEGHGGWVHSVAFSPDGQRVASGSIDGIIKIWDAASGICTQILEGHGGWV 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1070 SDDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIW 1120
                                                                                                                                                                                                                                                                                                                                                                                 950 KIWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHG 1009
                                                                                                                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGG-I 486
                                                                                                                                                                                                                                                                                     ANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD 190
                                                                                                                                                                                                                                                                                                       -----LEGHGGSVWSVAFSPDRERVASGSDD 904
                                                                                                                                                                                                                                                                                                                          STARIWNLSENSTSGS-TQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFA 249
                                                                                                                                                                                                                                                                                                                                                              250 RIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                    309 APALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC 367
                                                                                                                                                                                                                                                                                                                                     IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAASQQGSAKNGE-----NT
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             70;
                                                                                                                                                                                                          Length 1356;
                                                                                                                                                                                                                            73; Mismatches 178; Indels
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Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
                                                                                                                                                                                         965FB319844E0651 CRC64;
                                                                                                                                                                                                          ; DB 1;
3.3e-25;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
                                                                                    (POTENTIAL)
                                                                                                                                                                                                           Score 460;
Pred. No. 3
                        PROSITE; PS50837; NACHT; 1.
PROSITE; PS0678; WD REPRATS 1; 10.
PROSITE; PS50083; WD REPRATS 2; 10.
PROSITE; PS50284; WD REPRATS REGION; 1.
GTP-binding; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: | : | : | CSVAFSPDGQRVASGSSDKTIKIWD 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 FEVCWNAAGDKVGASASDGSVCVLD 511
                                                                                   GTP (1 WD 1. WD 2. WD 2. WD 4. WD 5. WD 6. WD 6. WD 6. WD 6. WD 6. WD 6. WD 9. WD 9. WD 10.
                                                                           NACHT
                                                                                                                                                                                        149765 MW;
PRINTS; PR00320; GPRCTEINBRPT.
ProDom; PD000018; WD40; 10.
SMART; SM00320; WD40; 10.
                                                                                                                                                                                                                                                                                                       ASG--TGTQT------
                                                                                                                                                                                                          16.9%;
27.9%;
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nes 124; Conservative
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                                                                                            869
911
953
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SEOUENCE FROM N.A.
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Q8YV57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 LASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDL
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto G., Elamentous M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1683;
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llarity 28.5%; Pred. No. 4.9e-24;
Conservative 69; Mismatches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; GPROTEINBRPT.
SMART; SMO0320; MP40; 14.
PROSTIE; PS00678; WD REPERTS 1; 3.
PROSITE; PS50082; WD REPERTS 2; 14.
PROSITE; PS50294; WD REPERTS 2; 14.
PROSITE; PS50294; WD REPERTS REGION; 1.
RYPOTHETICAL DIOCTEIN; Repeat; WD remeat
                                                                                                                                                                                                                             -! - SIMILARITY: Contains 13 WD repeats.
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PIR; AF2071; AF2071.
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Matches 109; Conserv
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TISSUB-Lung, and Placenta;

XX Staueberg From N.A.

XX Staueberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;

XX Staueberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;

XX Staueberg R.L.; Feingold B.A.; Grouse L.H.; Schemen C.M.; Schuler G.D.;

XX Altschul S.F.; Zeeberg B., Buetow K.H.; Scheefer C.F.; Bhat N.K.;

XX Altschul S.F.; Joedan H.; Moore T., Max S.I.; Wang J., Hableh F.;

XX Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.,

XX Stapleton M.J.; Usdin T.B.; Toshiyuki S., Carninot P., Prange C.;

XX Raha S.A.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

XX Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunarane P.H.;

XX Chards S., Worley K.C.; Hale S., Garcia A.M.; Gabs R.A.;

XX Norley K.C.; Hale S., Garcia A.M.; Gibbs R.A.;

XX Norley K.C.; Alale S., Garcia A.M.; Gibbs R.A.;

XX Norley K.W.; Touchman J.W.; Madan A., Rodrigues S., Sanchez A.,

XX Rodriguez A.C.; Grimwood J.; Schmutz J., Myers R.W.;

XX Rodriguez A.C.; Grimwood J.; Schmutz J., Marra M.A.;

XX Rodriguez A.C.; Grimwood J.; Schmutz J., Marra M.A.;

XX Generation and initial analysis of more than 15,000 full-length

XX Human and mouse CDNA sequences.";

XX Natl. All R. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                      278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                               338 QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI 397
                                                                                                                                                                                                                                                                                                          398 KWSPIGPGINNPNANLMLASASFDSIVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYL 457
158 PPNKAVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIRE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishia S., Muzakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human CDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUS7_HUMAN STANDARD; PRT; 485 AA. Q9NVZ; 060868, Q9BU54; 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) WD-repeat protein HUSSY-07.
                                                                                                                                                                                            1518 SRYİLTASVDNTARİWDF------
                                                                                                                                                                                                                                                                                                                                                                                                                         1645 LTSSADGTAKLWPVKT 1660
                                                                                                                                                                                                                                                                                                                                                                                   458 ASGSFDKCVHIWNTQT 473
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                                                                                                                                                                                                                                                                                                                                                                                       Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Sprechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D63999; BAA10064.1; -..

PIR; $76086; $76086.

InterPro; IPR0018941; TPR-like.

InterPro; IPR001899, WD40; 16.

PRINTS; PR00320; GPROTBINBRPT.

PRODOM; PD00019; WD40; 16.

PROSITE; PS00678; WD REPEATS.1; 8.

PROSITE; PS50082; WD REPEATS.2; 15.

PROSITE; PS50082; WD REPEATS.2; 15.

PROSITE; PS50094; WD REPEATS.2; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.3%; Score 388.5; DB 1; Length 1693;
Best Local Similarity 28.5%; Pred. No. 6.4e-20;
Matches 107; Conservative 52; Mismatches 138; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0977A827A0251CFF CRC64;
                                                                                                                                                                                                                                                             Bacteria, Cyanobacteria, Chrococcales, Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein s110163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 2:153-166(1995).
-!- SIMILARITY: Contains 16 WD repeats.
    1612 HQAGVMSAIFSPDGKTLISGSLD 1634
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3 WD 2.
4 WD 4.
6 WD 5.
7 WD 6.
38 WD 5.
10 WD 9.
11 WD 10.
11 WD 11.
52 WD 11.
53 WD 13.
116 WD 13.
116 WD 13.
                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803)
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1504
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Y163_SYNY3
Y1643_SYNY3
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REPEAT 10
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH-- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 IDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                     Sanchez J.-C.,
                                                      to
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                               Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B., Cannata N., Zimbello R., Lanfranchi G., Valle G., "Characterization of 16 novel human genes showing high similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 366.5; DB 1; Length 485; 26.8%; Pred. No. 4.7e-19; Live 47; Mismatches 145; Indels 89
                                                                                                                    К.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OAEBE24B44957379 CRC64;
                                                                                                          MEDLINE=22317277; PubMed=12429849; Scherl A., Coute Y., Deon C., Calle A., Kindbeiter K. Scherl A., Coute Y., Deon C., Calle A., Kindbeiter K. Greco A. Hochstrasser D.F., Diaz J.-J.; "Functional proteomic analysis of human nucleolus."; Mol. Biol. Cell 13:4100-4109(2002).
-i- SUBCELINILAR LOCATION: Nuclear; nucleolar.
-i- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS0082; WD_REPEATS_2; 7.
PROSITE: PS50294; WD_REPEATS_REGION;
Nuclear protein; Repeat, WD_repeat.
                     MEDLINE=21064499; PubMed=11124703;
                                                                                                                                                                                                                                                                                    EMBL, AKOO1320; BAA91621.1; -...
EMBL, BCO02884; AAH02884.2; -...
EMBL; BCO12075; AAH12075.1; -...
EMBL, AL005257; CAA6444.1; -...
SWISS-2DAGE; QONVX2; HUMAN.
InterPro; IPR001632; Gprotein_B.
InterPro; IPR001680; WD40.
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PRINTS; PR00319; GPROTEINB.
PRINTS; PR00320; GPROTEINBRT.
PRODOM; PD001018; WD40; 7.
SMART; SM00320; WD40; 8.
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451 WI
484 WI
53266 MW;
SEQUENCE OF 400-485 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103; Conservative
                                                               yeast sequences.";
Yeast 18:69-80(2001).
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                                                                                               SUBCELLULAR LOCATION
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197
244
325
370
412
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AA;
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Best Local 8
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                                                                                                                                             386 DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV 445
                                                                                                                                                                                                     SLRGHVAAVYQIAWSAD-----SRLLVSGSSDSTLKVWDVKAQKLAMDLPGHADEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Masinae; Marinae; Musinae; Masinae; 
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PRINTS; PR00120; GPROTEINB.
PRINTS; PR00120; WD40; 7.
PLODOM; PD000018; WD40; 7.
PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082, WD_REPEATS 2; 7.
PROSITE; PS50082, WD_REPEATS 2; 7.
NUCLEAR DIOLEGIN; REPEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                        446 YSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                                                                                                                                                                                                                                                                                                460 YAVDWSPDGQRVASGGKDKCLRIW 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932
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InterPro; IPR001632; Gprotein_
InterPro; IPR01680; WD40.
Ffam; PF00400; WD40; 8.
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MEDLINE=2284356; PubMed=1574125;
MEDLINE=92244356; PubMed=1574125;
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                                                                                                                                                                                                      165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                                                                                                                                                                                                                                                               230 VWDTTAGRCERILIGHTQSVTCLRWGGDG-LLYSASQDRTIKVWRAHDGVLCRTLQGHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 DDFILFIWSPAEDKKPLARMTGHQALINQVIFSPDSRIVASASFDKSIKLWDGRIGKYLA
                                                                                                                                                                                                                           221 DVPS-----NSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                       170 KLASGCKNGQILLWDPSTGLQVGRTLTGHSKWITGLSWBPLHMNPECRYVASSSKDGSVR
                                                                                                                                                                                                                                                                                                                                           IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH--
                                                                                                                                                                                                                                                                                                                                                                                                                                              289 WYNTWALSTDYALRTGAFEPAEATVNAQDLQGSLKELKERASSRYNLVRGQGPERLVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLLKHQEPV
                                                                                                                                                                     89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; Ascomyocta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                   Length 485;
                                                                                                                                                                     Indels
                                                                                                 2D7F59D603AEC07B CRC64;
                                                                                                                                     DB 1;
                                                                                                                                                                     48; Mismatches 145;
                                                                                                                                   Score 365.5; DB 1
Pred. No. 5.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCW2 YEAST STANDARD; PRT; 515 AA. P25382; QBNKJ4; 01-MAY-1992 (Rel. 22, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical WD-repeat protein YCR072C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 YAVDWSPDGQRVASGGKDKCLRIW 483
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WD 3.
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                                                                                                    53148 MW;
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 241
282
366
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481
                                                                                                    485 AA;
                                                                                                                                                       Similarity
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                                                                                                    SEQUENCE
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Best Local
REPEAT
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Lucchini G., Iutzenkirchen K., Maat C., Mannhaupt G., Manzano M.E.,
Martegani E., Mathieu A., Maurer C.T.C., McConnell D., McKee R.A.,
Messenguy F., Mewes H.-W., Molemans F., Montague M.A., Navas L.,
Newlon C.S., Olson M.V., Pallier C., Panzeri L., Pearson B.M.,
Perea J., Philippsen P., Parard A., Planta R.J., Plevani P.,
Poetsch B., Pohl F.M., Purnelle B., Ramazani Rad M., Rasmussen S.W.,
Raynal A., Remacha M., Richterich P., Roberts A.B., Rodriguez F.,
Sanz E., Schaaff-Gersenschaeger I., Scherns B., Schweitzer B.,
Shu Y., Skala J., Slonimski P.P., Sor F., Soustelle C.,
Sheglegelberg R., Stateva L.I., Steenswa H.Y., Steiner S., Thierry A.,
Thirocs G., Triano L.N., Urrestarauu L.A., Valle G., Vetter I.,
van Vliet-Reedijk J.C., Volckaert G., Vreken P., Warmington J.R.,
von Wettstein D., Micksteed B.L., Milson C., Wurst H., Xu G.,
I'The complete DNA sequence of yeast chromosome III.";
Nature 357:38-46(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 365.5; DB 1; Length 23.2%; Pred. No. 6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jimenez A., .
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valles G., Volckaerts G.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 8 WD repeats.
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PIR; S19487; S19487; CAC42989.1; -
GermOnline; 138973; -
GermOnline; 138973; -
GermOnline; 138973; -
GermOnline; 138973; -
GermOnline; 138073; -
InterPro; IPR001632; Gprotein_B.
PROM: PR000168; W440.
PRINTS; PR00130; GPROTEINB.
PRINTS; PR00130; GPROTEINB.
PRINTS; PR00130; GPROTEINB.
PROSTITE; PS00678; WD REPEATS 1; 5: PROSITE; PS00678; WD REPEATS 2; 7: PROSITE; PS500294; WD REPEATS REGION; 1.
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57025 MW;
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Matches 124; Conservative
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484
515 AA;
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                                                                                                                                                                                                                                                                                                                         ----NNPNANLMLASASFDSTVRLWDVDRGI-CIHTLTKHQEPVYSVAFSPDGRYLASG 460
-----IAGHGSTILCSAFAPHTSSRMVTGAGDNTARIWDCDTQTPMH 180
                                                                      -----SWSPDGEVIATGSMDNTIRLWDPKSGQCLG 222
                                                                                                         312
                                                                                                                                                                                                    STSGSTQLVLRHCIREGGDDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW-TKDGN-LA
                                                                                                       STLGQHKGPIFALKWN-----KKGN--FILSAGVDKTTIIWDAHTGEAKQQFPFHSAPAL
                                                                                                                                                                               313 DVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMT
                                                                                                                                                                                                                                                                                    VRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKPSTPEEAQKKALENY
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"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters casparagine, glutamine, or threonine.";
Mol. Gen. Genet. 218:453-459(1989).
-! - DEVELOPMENTAL STAGE: The concentration of AAC-rich mRNAs is low
                                                                                                                                                                                                                                                                                                                                                                                                                  SFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDLR 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in dormant spores and growing cells, but increases during spore-germination and multicellular development.
MISCELIANEOUS: Several proteins derive from AAC-rich mRNA, whi due to a frameshift also have ACA and CAA codons and thus are Asn-, Thr- or Gln-rich.
                                                                                                                                           DALRGHSKWITSLSWEPIHLVKPGSKPRLASSSKDGTIKIWDTVS----
                                                                                                                                                                                                                                                    373 LKIWSM-KQDNCVHDLQQHNKEI-----YTIK---WSPTG--PGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-YAR-2004 (Rel. 43, Last annotation update)
AAC-rich mRNA clone AAC3 protein (Fragment).
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SMART; SNO0320; MD40; 5.
PROSITE; PSO0678; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 7 WD repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=90066348; Pubmed=2511421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X16524; CAA34531.1; -.
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 5.
                                                                  TLKGHYNWVL--CV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 PCRSVSFSFDGQFIAASSFESTIEIFHIESSQPIHTIE-CSGVSSLMWHPTLPLLAYAPE
                                                                                                                                                                                                                     --TKDGNLAST--LGQHKGPIF
                                                                                                                                                                                                                                                                               132 WNANGTKIASSGSDGIVRVWNFDPLGNSNNNNSNNTSSNSKNNNIKETIELKGHDGSIE
                                                                                                                                                                                                                                                                                                         271 ALKWNKKGNFIL-SAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTF-ASCSTD
                                                                                                                                                                                                                                                                                                                              192 KISWSPKNNDLLASAGTDKVIKIWDVKIGKCIGTVSTNS-ENIDVRWSPDGQFIVACTRD
                                                                                                                                                                                                                                                                                                                                                         329 MCIHVCKLGQDRPIKTFOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH---
                                                                                                                                                                                                                                                                                                                                                                                                            386 --DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQE
                                                                                                                                                                                                      180 VSDLLASGSGDSTARIWNLSENST-----SGSTQLVLRHCIREGGQD-VPSNKDVTSLD
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                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98225157; PubMed=9556563;
Johnstone R.W., Wang J., Tommerup N., Vissing H., Roberts T.,
"Ciaol is a novel WB40 protein that interacts with the tumor
suppressor protein WT1.";
J. Biol. Chem. 273:10880-10887(1998).
                                                                                                                                                   Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Loftus B.J., Zhou L., Crosby M., Fuhrmann J., Brandon R., Kim U.J., Kerlavage A.R., Venter J.C., Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             Indels
                                                                                                                           7B5AE61228D0A1A9 CRC64;
                                                                                                                                                  12.8%; Score 348.5; DB 1; 26.1%; Pred. No. 8.1e-18; ive 72; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
WD-repeat containing protein Clao 1.
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WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
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                                                                                                                            49151 MW;
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421 INENNKDPSIRV 432
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Best Local Similarity
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or send an email to license@isb-sib.ch).
MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J. Gares M.B., Bonaldo M.F., Casarant T.L., Scheetz T.E.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodersten E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.;
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008284; P:positive regulation of cell proliferation; TAS. GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS. InterPro; IPRO01689; WD40. Pfam. PP00400; WD40; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=99367400; PubMed=10438340;
Medline=99367400; PubMed=10438340;
Ochnetone R.W., Tommerup N., Hansen C., Vissing H., Shi Y.;
Johnstone R.W., Tommerup N., Hansen C., Vissing H., Shi Y.;
Structural organization, tissue expression, and chromosomal localization of Ciao 1, a functional modulator of the Wilms' tumor suppressor, WTI.";
Immunogenetics 49:900-905(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Seems to specifically modulate the transactivation activity of WT1.
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-i- MISCELLANEOUS: 'Ciao' means 'bridge' in Chinese.
-i- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
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WD 3.
WD 4.
WD 5.
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EMBL, AAC04020; AAC23493.1; -.
EMBL, BCC001395; AAH801395.1; -.
EMBL, BC032812; AAH32812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT.
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SM00320; WD40; 7.
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80; Gaps

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EIYTIKWSPIGPGINNPNANLMLASASFDSTVRLW--DVDRGICIHTLTKHQEPVYSVAF 450
                                                                    KKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCK 335
                                                                                                                                                                         -----TLEGHENEVKSVAWAPSGNLLATCSRDKSVWVWEVDEEDEYECVSVLNSHTQ 151
                                                                                                                                                                                                                                                222 VPSNKDVTS--LDWNSEGTLLATGSYDGFARIWTKDGN---LASTLGQ-HKGPIFALKWN 275
                                                                                                                                                 336 LGQDRPIKTPQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDN---CVHDLQQHNK 392
                                                                                                                                                                                                                                                                                               SPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGS---V 507
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                                     11 VPAHPDSRCWFLAWNPAGTLLASCGGDRRIRIWGTEGDSWICKSVLSEGHQRTVRKVAWS 70
                                                                                                            ---WKKNODDFECVT-----
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Job time : 18.6667 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec

Title: Perfect score:

US-09-987-701-12 2731 1 MSISSDEVNFLVYRYLQSSG......GDKVGASASDGSVCVLDLRK 514 Sequence:

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

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                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                           DB 1; Length 514;
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-> H (IN REF. 3).
-> Q (IN REF. 2).
0B556D2EE4BA796D CRC64;
                                                                                                                                                                                                           Score 2696; DB 1;
Pred. No. 5.7e-188;
1; Mismatches 5;
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     PROSITE; PS50896; LISH; 1.
PROSITE; PS06791 ND REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                       LISH.
WD 1.
WD 2.
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WD 6.
WD 7.
WD 8.
T > M (III
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                                                 Repeat; 1
DOMAIN
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                                                                                                                                                               CONFLICT
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16-OCT-2001 (Rel. 40, Created)
By FFB--2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amocation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)

526 AA

TBLX HUMAN 060907;

DT DT DT OCS

TBLIX OR TBLI. Homo sapiers (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

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RA KISUSELYMPDA,

RA KISUSELYMPDA,

RA STERUSDEST, PubMed=12477932;

RA KISUSSELY, Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Sthain G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

R. Helton E., Ketteman M., Madan A., Robrigues S., Banchez A.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

- TISSUE SPECIFICITY: Ubiquitous C. - SIMILARITY: Contains 8 WD repeats.
                                                                                                             MEDLINE-99264241; PubMed-10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.; "X-linked late-onset sensorineural deafness caused by a deletion involving OAl and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616 (1999):
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0007605; P:hearing; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007601; P:vision; TAS.
InterPro; IPR001689; Lish.
InterPro; IPR001689; W40.
PED: PR00100; W040; B.
PRINTS; PR00120; GPROTEINBRPT.
PR000018; W409; 3.
SWART; SW0067; Lish; 1.
SWART; SW001018; W409; 7.
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PROSITE; PS00678; WD REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL, BC032708; AAH32708.1; -.
Genew, HGNC:11585; TBL1X.
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
276
318
359
401
452
                                            NCBL_TaxID=9606;
                                                                                                      SEQUENCE
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                                                                                                                                        61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAT-- 118
                                                                                                                                                      179
                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                             239
                                                                                                                                                                                                                                                                                    287
                                                                                                                                                                                                                                                                                               KTT11WDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQG 347
                                                                                                                                                                                                                                                                                                                                            HINEVNAIKWDPSGMLLASCSDDMTLKIWSMKOEVCIHDLOAHNKEIYTIKWSPIGPAIS 419
                                                                                                                                                                                                                                                                                                                                                                            HINEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTN 407
                                                                                                                                                                                                                                                                                                                                                                                                                          NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVH 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPNSNIMLASASFDSTVRLWDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVH 479
                                                                                                                   9
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                                                                                                          ------NQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRG
                                                                                                                                                                                                     HESEVFICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPSNKD
                                                                                                                                                                                                                                                         HESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKD
                                                                                                                                                                                                                                                                                 VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD
                                                                                          1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
                                                                      Gaps
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
TBL1Y OR TBL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rozen
                                                526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWNTOSGNLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown L.G.,
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK
                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuroda-Kawaguchi T., Skaletsky H., Minx P.J., Brown L.G. Wilson R.K., Waterston R.H., Page D.C.; "The DNA sequence of the human Y chromosome."; Submitted (DEC-2000) to the EMBJ/GenBank/DDBJ databases.-!- SIMILARITY: Contains 1 LisH domain.
            POLY-ALA.
98922F88EC42F6E9 CRC64;
                                            ; Score 2439; DB 1; 1; Pred. No. 2.5e-169; 33; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522 AA
  ΜĐ
 525 WD
124 PO
57048 MW;
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                             89.3%;
86.0%;
                                          Query Match
Best Local Similarity 86.0
Matches 453; Conservative
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493
108
526 AA;
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HUMAN
TBLY_HUMAN
REPEAT
DOMAIN
SEQUENCE
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115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 SEVFICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIIWDAHTGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 TIIWDAHTGEAKQQFPFHSAPALDVDWQNNMTFASCSTDMC1HVCRLGCDHPVKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AATNOOGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 NSSIMLASASFDSTVRLWDVEÇGVCTHTLMKHQEPVYSVAFSPDGKYLASGSFDKYVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 NEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 NEVNAIKWDPSGMLLASCSDDWTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTGPATSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 NANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                              LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
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WD 6.
WD 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 NTQSGSLVHSYQGTGGIFEVCWNARGDKVGASASDGSVCVLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.1%; Score 2351; DB 1;
ilarity 83.9%; Pred. No. 5.9e-163;
Conservative 35; Mismatches 37;
                                                                                                                                                                                                                                                                                                             i
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                               PROSITE; PSS0896; LISH; 1. 4. PROSITE; PSS0878; WD REPEATS 1; 4. PROSITE; PSS0082; WD REPEATS 2; 6. PROSITE; PSS0294; WD REPEATS REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                   EMBL, AF332220, AAK13472.1; -.
EMBL, AF332221, AAK13473.1; -.
EMBL, AF332222, AAK13474.1; -.
Genew, HGNC:18502, TBLIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56688 MW;
                                                                                                             InterPro; IPRO06594; LisH.
InterPro; IPRO01680; WD40.
Pfam; PF00400; WD40; B.
PRINTS; PR00320; GPROTEINBRPT
                                                                                                                                                                                   Prodom, PD000018; WD40; 3.
SWART; SM00667; LisH; 1.
SWART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 439;
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STANDARD;

STANDARD;

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SIF2 YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 MLLASCSDDMTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTGFATSNPNSNIMLASASFD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 SGDSTARIWNLSENSTSGPTQLVLRHCIREGGODVPSNKDVTSLDWNSEG----TLLAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 GSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 NILASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFPFHS-APALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SGDSTARIUMLNENSNGGSTQLVLAHCIREGGHDVPSNKDVTSLDWNMEHCWQQVPMMVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Buthéria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 STVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIVRLWDVERGVCIHTLIKHQEPVYSVAFSPDGKYLASGSFDKCVHIWNIQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                 Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston Hunter G., Kimberly C., Rhodes M.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: Contains at least 5 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 1304; DB 1; Length 313; 83.2%; Pred. No. 2.3e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34808 MW; 3BC48683432DFEF7 CRC64;
                      10-OCT-2001 (Rel. 40, Last sequence update)
Transducin beta-like 1X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.3e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00320; WD40; 5.
PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50062; WD REPEATS 2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M M D 2.
M M D 3.
M M 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 5.
PRINTS; PR00320; GPROTEINBRPT.
Probom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; F38006; CAB61534.1; -.
MGD; MGI:1336172; Tbllx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.28
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 3
313 AA;
                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat, WD repeat.
NON TER 1
REPEAT <1
REPEAT 76 1
REPEAT 160 1
                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=129/SvJ;
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SEQUENCE
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RESULT 5 SIF2\_YEAST

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MEDINE=21567937; PubMed=11711434;

Whilm M., Rigaut G., Seraphin B., Asadland R., Stevchenko A., Tekotte H.,

Milm M., Rigaut G., Seraphin B., Asadland R., Stewart A.F.;

Milm M., Rigaut G. Seraphin B., Asadland R., Stewart A.F.;

Milm M., Rigaut G., Seraphin B., Asadland R., Stewart A.F.;

Milm M., Rigaut G., Seraphin B., Asadland R., Stewart A.F.;

Milm M., Rigaut G., Seraphin B., Asadland R., Stewart A.F.;

More Drogram.";

Gene program.";

Gene Drogram.";

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GO: GO:0001718; P:nab-dependent histone deacetylase activity; IDA.
GO: GO:0017186; P:NAb-dependent histone deacetylase activity; IDA.
GO: GO:006518; P:NAb-independent histone deacetylase activity; IDA.
GO: GO:006518; P:NAb-independent histone deacetylase activity; IDA.
GO: GO:0016575; P:histone deacetylation; IDA.
GO: GO:00122; P:histone deacetylation; IDA.
GO: GO:000122; P:negative regulation of transcription from P. . .; IPI.
InterPro: IPRO01680; Mu40.
PFO0400; WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95208357; PubMed=7900426;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION IN A COMPLEX WITH HOS2; HST1; SNT1; CPR1; YIL112W AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98315485, PubWed=9651685,
Cockell M., Renauld H., Watt P., Gasser S.M.;
"S1f2p interacts with Sir4p amino-terminal domain and antagonizes
                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                   (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; P0000018; WD40; 1.
SWART; SW00667; LisH; 1.
SWART; SW008320; WD40; 4.
SWART; EPS0896; LISH; 1.
PROSITE; PS00678; WD REPEATS_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X78993; CAASS606.1; -.
EMBL; Z35972; CAA85058.1; -.
PIR; S48268; S48268.
Germonline; 138646; -.
SGD; SANANAAA.
                                                                                                                                         SIR4-interacting protein SIF2.
SIF2 OR EMB1 OR YBR103W OR YBR0832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               telomeric silencing in yeast.";
Curr. Biol. 8:787-790(1998).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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CHARACTERIZATION.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                   01-OCT-1994 (
01-OCT-1994 (
10-OCT-2003 (
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                                                                                                                                                                                                  VEAEVSINEDG----TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAA 116
                                                                                                                                                                                                                 TESELMVDSKGDISALNEHHLSEDFNLVQALQID-----KEKFPE--ISSEGRFTL 109
                                                                                                                                                                                                                                                                                                                                                                                            344 YQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSGNSFYGHSQS 403
                                                                                                                                                                                                                                                                                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATNOQGSAKNGENTANGEENGAHTIANNHTDMM-EVDGDVEIPSNKAVVIRGHESEVFIC 175
                                                                                                                                                                                                                                                      110 ETNSE-SNKAGEDGASTVERETQEDDTNSIDSSDDLDGFVKI--LKEIV---KLDNIVSS 163
                                                                                                                                                                                                                                                                                         TWNPLDESILAYGEKNSVARLARIVETDQEGKKYWKLTIIAELRHPFALSASSGKTTNOV 223
                                                                                                                                                                                                                                                                                                            TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDK 288
                                                                                                                                                                                                                                                                                                                      TCLAWSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWKDGTHIISMDVEN 283
                                                                                                                                                                                                                                                                                                                                              TIIIWDAHTGEAKQQFPF------HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                                   CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                     IVSASWV------GDDKVISCSMDGSVRLWSLKONTLLALSIVDGVPIFAGRISOD 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VHSYRGTGGIFEVC 490
                                                                                                                                                                        1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNIN-GALVPPAALISIIQKGLQY
                                                                                                                                                                                                                                                                        176 AWNPVSD-LLVSGSGDSTARIWNLSENSTSGPTQ-----LVLRHCIREGGQDVPSNKDV
                                                                                                                                                                                                                                                                                                                                                               284 VTILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV
                                                                                                                                                                                                                                                                                                                                                                                                                     IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD
                                                                                                                                                Gaps
                                                                                                                                              79;
                                                                                                                             DB 1; Length 535;
                                                                                                 -> C (IN REF. 1; CAA85058)
25DD19AB2BFB4B07 CRC64;
                                                                                                                                               Mismatches 239; Indels
WD_REPEATS_2; 4.
WD_REPEATS_REGION; 1.
Chromatin_regulator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRYLASGSFDKCVHIW-----NTQTGAL------
                                                                                                                            18.4%; Score 501.5; DB 1 25.4%; Pred. No. 6.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
WD-repeat protein alr3466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1526 AA
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                                    WD 1.
WD 3.
WD 4.
WD 5.
WD 6.
WD 6.
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                                                                                                                                             Conservative 101;
                                                                                                           59145 MW;
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479
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535 AA;
PS50082; W
                   WD repeat;
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Best Local Similarity
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SEQUENCE FROM N.A.
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Anabaena sp.
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                                                                                                                                            Matches 143;
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28-FEB-2003
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Q8YRI1;
PROSITE;
PROSITE;
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                    Repeat;
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                           DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 -TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFFFHSAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGAHTIANNHTDMMEVDGDVEIPSNKAV-VLRGHESEVFICAWNPVSDLLVSGSGDSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 IWNLSENSTSGPTQLVLRHC--IREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 LWDISSSK------CLYILQG----HTSWVNSVVFNPDGSTLASGSSDQTVRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1228 BINSSKCLCTFQGHTSWNSVVFNPDGSMLASGSSDKTVRLWDISSSKCLHTFQGHT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 LDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 ASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                    Kaneko I., Nakamura Y., Wolk C.P., Kuritz I., Sasamoto S., Nakanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabara S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8:205-213 (2001).

-! SIMILARITY: Contains 16 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1526;
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30.3%; Pred. No. 8.6e-27;
tive 77; Mismatches 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PÉGN; PP00400; WD40; 15.
PRINTS; PR00120; GPROTEINBRPT.
PRODOM; PD000018; WD40; 8.
SYART; SW00320; WD40; 15.
PROSITE; PS00678; WD REBEATS 1; 11.
PROSITE; PS50082; WD REBEATS 1; 11.
PROSITE; PS50083; WD REBEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WD 1.
PENTAPEPTIDE
MEDLINE=21595285; PubMed=11759840;
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InterPro, IPR007111, NACHT NTPase.
InterPro, IPR001680; WD40.
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8 1447 WD 15
0 1491 WD 16
6 AA; 170376 MW; 1
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Conservative 7
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1240
1282
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Best Local Simi
Matches 118;
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1356 AA; 149765 MW; 965FB319844E0651 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical WD-repeat protein air2800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain PCC 7120)
                                                                                     Matches 121; Conservative
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                                                                  Similarity
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      SEQUENCE
                                                 Query Match
                                                                      Local
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AC 28-FEB

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DT 10-FEB

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OC Bacter

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CC 1---

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        1452
                                                                    RLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNIQIGALVHSYRG-T 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE 90009991; PubMed=7557402; Saupe S. Turcq B., Begueret J.; Saupe S., Turcq B., Begueret J.; A gene responsible for vegetative incompatibility in the fungus bedospora anserina encodes a protein with a GTP-binding motif and G beta homologous domain."; Gene 162:132-193 (1995).

-i. FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
                                                                                            1393 RLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLWNISSGECLYTLHGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetatible incompatibility protein HET-E-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                             484 GGIFEVCWNAAGDKVGASASDGSVCVLDLR 513
                                                                                                                                                                                                                                                                                                PRT; 1356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 NACHT domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM0330; WD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS50878; WD REPEATS 1; 10.
PROSITE; PS50082; WD REPEATS 2; 10.
PROSITE; PS50294; WD REPEATS REGION; 1.
GTP-binding; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 10 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 128125; AAA85775.1;
PIR, T18521; T18521.1
InterPro; 1978007111; NACHT_NTPase.
InterPro; 19780071680; WD40.
Pfam; PP05729; NACHT; 1.
Pfam; PP00400; WD40; 10.
PRIM; PP00300; GPROTEINBRPT.
PRODOM; PD000018; WD40; 10.
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                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Podospora anserina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                     PODAN
                                                                          425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NP BIND
REPEAT
                                                                                                                                                                                                                                                                                                   HET1 PC
Q00808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1011 SVWSVAFSPDGQRVASGSDDKTİKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGS 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1071 DDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIWD 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122 AASGICTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGICTQTLEGHGGWVQ 1181
                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                                                                         STARIWNLSENSISGPIQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLAIGSYDGFAR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 KTIKIWDAASGTC---TQTLEGH----GGR-----VQSVAFSPDGQRVASGSDDHTIK 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 VDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGG-IF 487
                                                                                                                                                                                                                            870
                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAATNQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWD
                                                                                                                                                                                                                    820 ISTISVVEÅEWNACTOT-----LEGHGSSVLSVÅFSADGORVÅSGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                              131 ANGEENGAHTIANNHIDMMEVDGDVEIPSNKAVVLRCHESEVFICAWNPVSDLLVSGSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 PALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCS
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENTE FROM N.T.

MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsumo A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Vasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120.";

In SIMILARITY: Contains 1 NB-ARC domain.

-: SIMILARITY: Contains 15 WD repeats.
                                                                             68;
       Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
16.9%; Score 462; DB 1; Length 13 27.3%; Pred. No. 1.7e-25; ive 74; Mismatches 181; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .552 KTVKLWRSHDGHLLHTFSGHSNVVYSSSFSPDGRYIASASEDKTVKIWQIDGHLLTTLPQ 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPVSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 LVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 QPPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TFTGHSGGVYAVNFLPDSNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                               Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEGM; PF00400; WD40; 14.

PRINTS; PR00320; GPROTEINBRPT.

PROSITE; PS00679; WD REPEATS 1; 3.

PROSITE; PS500294; WD REPEATS 2; 14.

PROSITE; PS50294; WD REPEATS REGION; 1.

Hypothetical protein; Repeat; WD repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F7CB361FF54F7137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 451; DB 1;
Pred. No. 1.5e-24;
                                                                                                                                                                                                         cyanobacterium Anabaena sp. strain PCC 7120.",
DNA Res. 8:205-213(2001).
-!- SIMILARITY: Contains 13 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%; scc. No. 1...
28.5%; Pred. No. 1...
71; Mismatches 1
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      MEDLINE=21595285; PubMed=11759840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003588; BAB73823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JR; AF2071; AF2071.
InterPro; IPR001680; WD40.
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Matches 109; Conservative
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1609
1650
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11320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFSPDGK-----ILASASHDQTVRIWDVNTGKCHHICIGHTHLVSSVAFSPDGEVV 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 KWSPIGPGINNPNANLMLASASFDSTVRLWDVDRGICIHTLITKHQEPVYSVAFSPDGRYL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 LRGHESEVFICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LRGHSNRVYSALFSPNGEIIATCSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77;
                      PIR; A12155; A12155.

InterPro; IPR001609; WD-ARC.

InterPro; IPR001609; WD-4C.

Pfam; PF00031; NB-ARC; 1.

PFINITS; PR00320; WD40; 14.

PRINTS; PR00320; WD40; 1.

PROSITE; PS000018; WD-REPEATS 1; 9.

PROSITE; PS50082; WD-REPEATS 2; 14.

PROSITE; PS50084; WD-REPEATS 2; 14.

PROSITE; PS50294; WD-REPEATS 2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 459.5; DB 1; Length
; Pred. No. 2.4e-25;
44; Mismatches 101; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45DF03B91170C451 CRC64;
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
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31.5%;
   AP003590; BAB74499.1;
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Best Local Similarity
Matches 102; Conserv
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SEQUENCE FROM N.A.
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Q8YV57;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEĞUENCE FROM N.A. Rabbada-8590279; Mablines 2017579; Mablines 2017529; Pubbada-8590279; Marabines 2017529; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
NCBI_TaxID=1148;
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; Pred. No. 3.6e-20;
53; Mismatches 137;
                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein sll0163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D63999; BAA10064.1; -.
PIR; S76086; S76086.
InterPro; IPR008941; TPR-like.
InterPro; IPR001689, WD40.
PÉAM, PF00400; WD40, 16.
PRINTS; PR00320; GPROTEIRBRPT.
PRODOM; PD000018; WD40; 13.
SWART; SM00320; WD40; 13.
PROSITE; PS50082; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS 2; 15.
PROSITE; PS500824; WD_REPEATS REGION; 1.
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SIMILARITY: Contains 16 WD repeats.
1612 HQAGVMSAIFSPDGKTLISGSLD 1634
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Best Local Similarity
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DNA Res. 2:153-1
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15-JUL-1998
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RR STRAIN-S2886;

RATAIN-S2886;

RATAIN-S2886;

RATAIN-S2886;

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RA Alberghina L., Alterandraki D., Antonie G., Anwar R., Bailesta J.P.G.,

RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A.,

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RA Kleinhans U., Kreisl P., Lafranchi G., Mannhaupt G., Manzano M.E.,

RA Mercgani E., Mathieu A., Maurer C.T. C., McConnell D., McKee R.A.,

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RA Zhimermann P.K., Sgourcs J.G.,

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RA Three G., This H. Sequest C., Vurkeken P., Warmigton J.R.,

RITHE C. M. Wartstein D., Wicksteed G., Willer G., Willer G., Willer G., Willer G., Willer G., 
                                  1415 ---KKLTVLRGHQDAVLNVR-SPDSQYIVTASKDGTARVWN-----NTGRELAVLRH---- 1463
                                                                                                                                                                    1464 -----YEKNIFAAEFSADGQFIVTASDDNTAGIWEIVGREVGICRGHEGPVYFAQFSAD 1517
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158 PSNKAVVLRGHESEVFICAMNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIRE 217
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Bukaryota, Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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10-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
47ypotchetical WD-repeat protein YCR072C.
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                             Jimenez A.;
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                                                                                        Valles G., Volckaerts G.,
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Pred. No. 8.8e-20;
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Germonline; 138973; -.

Germonline; 138973; -.

Germonline; 138973; -.

Germonline; 138973; -.

InterPro; IPR001662; Gprotein_B.

InterPro; IPR001660; Wb40.

PRINTS; PR00319; GPROTEINB.

PRINTS; PR00320; GPROTEINB.

PROMONT; SM00320; WD40; 8.

PROSITE; PS00678; WD_REPEATS 1; 5.

PROSITE; PS00629; WD_REPEATS 1; 5.

PROSITE; PS00629; WD_REPEATS 1; 5.

PROSITE; PS00629; WD_REPEATS 1; 5.

PROSITE; PS00629; WD_REPEATS 1; 5.

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WD 22.
WD 44.
WD 55.
WD 77.
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515 AA;
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Matches 125;
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                                                         464
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305 DINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKPSTPEEAQKKALENYEKIC 364
                                                                                                365 KKNGNSEEMMVTASDDYTMFLWNPLKSTKPIARMTGHQKLVNHVAFSPDGRYIVSASFDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       SIKLWDGRDGKFISTFRGHVASVYQVAWSSDCRLLVSCSKDTTLKVWDVR 474
                                                                                                                                                                      465 CVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
WD-repeat protein HUSSY-07.
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Proc. Natl. Acad. Sci.
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Yeast 18:69-80(2001).
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Cannata N.
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NCBI_TaxID=10090;
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HUS7 MOUSE
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is nn no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QSNNTFASCS 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IW-TXDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH--
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MOI. Biol. Cell 13:4100-4109(2002).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00320; WD40; B.
PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Nuclear protein; Repeat; WD_repeat.
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460 YAVDWSPDGQRVASGGKDKCLRIW 483
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                                                                                                                                                                                                                                                                                                                                     EMBL; AK001320; BAA91621.1; ---
EMBL; BC002084; AAH02084 2; --
EMBL; BC012075; AAH12075.1; --
EMBL; AL005257; CAA06444.1; --
SWISS-2DPAGE; Q9NVX2; HUMAN.
InterPro; IPR001632; Gprotein_B.
InterPro; IPR001632; Gprotein_B.
PRINTS; PR00199; WD40; B.
PRINTS; PR00199; GPROTEINB.
PRODOM; PD0000018; WD40; 7.
SWART; SM00320; WD40; 8.
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Matches 102; Conservative
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485 AA;
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MEDLINE-22388257; PubMed=12477932;

MISTALINE-22388257; PubMed=12477932;

MISTALINE-22388257; PubMed=12477932;

MISTALINE-22388257; PubMed E.A., Grouse D.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MISTALINE R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MISTALINE A., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MISTALINE A., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MISTALINE A., MocMan P.J., McKerran R.J., Maramon R.D., Mullahy S.J.,

MISTALINE A., MocMan P.J., McKerran R.J., Maramon R.D., Mullahy S.J.,

MISTALINE A., MocMan P.J., McKerran R.J., Maramon P.H.,

MISTALINE A., MocMan P.J., McKerran R.J., Maramon P.H.,

MISTALINE A., MocMan P.J., McKerran R.J., Maramon P.H.,

MISTALINE A., Mully D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Modan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Muterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Munan and mouse cDNA sequences.",

Mullalon D.C., Sunchains W WD repeats,

Mullalon D.C., Sunchains W WD repeats,

Mullalon D.C., Sunchains W WD repeats,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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13.3%; Score 362.5; DB 1; Length 485;
Best Local Similarity 26.3%; Pred. No. 7.1e-19;
Matches 101; Conservative 48; Mismatches 146; Indels 89;
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                                                    Last sequence update)
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PRINTS; PR00119; GPROTEINB.
PRINTS; PR00120; GPROTEINBRPT.
ProDom; PD000018; WD40; S.
SMART; SM00320; WD40; 8.
PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS5006294; WD REPEATS 2; 7.
PROSITE; PS500294; WD REPEATS REGION; 1.
Nuclear protein; Repeat; WD repeat.
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(Rel. 42, Created)
(Rel. 42, Last seq
                                          MD-repeat protein HUSSY-07.
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454
485 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLRGHVAAVYQIAMSAD-----SRLLVSGSSDSTLKVWDVKAQKLATDLPGHADEV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 DLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV 445
LEGHSEAVISVAFSPTGKYLASGSGDTTVRFWDLSTETPHFTCKGHRHWVLSISWSPDGK 169
                                                                                                                                                                                                        251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH-- 307
                                                                                                               --SAPALDVDW----OSNNTFASCS
                                                                                                                                                                                                                                                                                                                                                                                                                    289 WINTMALSTDYALRIGAFEPAEATVNAQDLQGSLKELKERASSRYNLVRGQGPERLVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH
                                                                  -----NKDVTSLDW-----NSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shaw D.R., Richter H., Giorda R., Ohmachi T., Ennis H.L.;
"Nucleotide sequences of Dictyostellum discoideum developmentally
"Nucleotide sequences of Dictyostellum discoideum developmentally
asparagine, glutamine, or threonine.";
Mol. Gen. Genet. 218:453-459 (1989)
-!- DEVELOPMENTAL STAGE: The concentration of AAC-rich mRNAs is low
in dormant spores and growing cells, but increases during
spore-germination and multicellular development.
-!- MISCELLANEGUS: Several proteins derive from AAC-rich mRNA, which,
due to a frameshift also have ACA and CAA codons and thus are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-YAR-2004 (Rel. 43, Last annotation update)
AAC-rich mRNA clone AAC3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINBRPT.
SWART; SW00320; WD40; 5.
PROSITE; PS00678; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asn-, Thr- or Gln-rich.
SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 YSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:| :||||: :||| XAVDWSPDGQRVASGGKDKCLRIW 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90066348; PubMed=2511421;
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InterPro, IPR001680, WD40.
Pfam, PF00400, WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                               DVPS----
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P14197;
110
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AAC3_DICODI
D AAC3_DICODI
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DT 01-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 LDLASRYFSECSTKDFIGNKKKSTSVAWNANGTKIASSGSDGIVRVWNFDPLGNSNNNNN 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 QFPFHSAPALDVDWQSNNTF-ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 AGSADSIVSLWDIEDMMCVKTFIKSTFPCRSVSFSFDGQFIAASSFESTIEIFHIESSQP 394
                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TKDGNLAST--LGQHKGPIFALKWNKKGNFIL-SAGVDKTTIIWDAHTGEAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 SNNTSSNSKNNNIKETIELKGHDGSIEKISWSPKNNDLLASAGTDKVIKIWDVKIGKCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 GDVEIPSNKAVVLRGHESEVFICAMNPVSDLLVSGSGDSTARIWNLSENST----SGP
                                                                                                                                                                                                                                                                                                                                                                                                                       -----NSNSKEST----NIPKTNTOYTNFDSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 NILASCSDDMTLKIWSMKQDNCVH-----DLQAHNKEIYTIKWSPTGPGTNNPNANLMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 SASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGAL
                                                                                                                                                                                                                                                                                                                                          28 QTQVQQLHNQLHQQHQQIQQQQQQQQHLQTQQYLQSQIHQQSQQSQLSNN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 TQLVLRHCIREGGQD-VPSNKDVTSLDWNSEGTLLATGSYDGFARIW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuhrmann J., Mason T.M., J.C.;
                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                   96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98225157; PubMed-9556563; Johnstone R.W., Wang J., Tommerup N., Vissing H., Roberts T., "Claol 1 is a lovel W040 protein that interacts with the tumor suppressor protein W11.";
                                                                                                                                                                                                                            Length 437;
                                                                                                                                                                                      7B5AE61228D0A1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 IHTIE-CSGVSSLMWHPTLPLLAYAPEINENNKDPSIRV 432
                                                                                                                                                                                                                                                                 79; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 VHSYRGTGGIFEVCWN-----AAGDKVGASASDGSVCV
                                                                                                                                                                                                                          ; DB 1;
1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
WD-repeat containing protein Ciao 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.J., Zhou L., Crosby M.,
J., Kerlavage A.R., Venter
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                                                                                                                                                                                                                          13.1%; Score 358; 23.7%; Pred. No. 1
                                  WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
GLN-RICH.
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                            161 WI
227 WI
326 WI
308 WI
355 WI
397 WI
49151 MW
                                                                                                                                                                                                                                               Best Local Similarity 23.7
Matches 109, Conservative
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Adams M.D., Loftus B.J
Brandon R., Kim U.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                      437 AA;
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WD repeat
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316
358
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REPEAT
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                                     TISSUEBLOOG, and SKID;

KINDLINE=22388257; PubMed=12477932;

KINDLINE=22388257; PubMed=127;

KINDLINE=223882657;

KINDLINE=22382657;

KINDLINE=22382657;

KINDLINE=22382657;

KINDLINE=2238265;

KINDLINE=22382665;

KINDLINE=223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnstone R.W., Tommerup N., Hansen C., Vissing H., Shi Y., "Structural organization, tissue expression, and chromosomal localization of Ciao 1, a functional modulator of the Wilms' tumor suppressor, WTI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 49:900-905(1999).
-!- FUNCTION: Seems to specifically modulate the transactivation activity of WT1.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63A8D8257A204FC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Interacts with WT1.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: 'Ciao' means 'bridge' in Chinese.
-!- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00679; WO.REPEATS_1; 1.
PROSITE; PS50082; WD.REPEATS_2; 6.
PROSITE: PS50294; WO.REPEATS_REGIO; 1.
Repeat; WD.repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE=99367400; PubMed=10438340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC004020; AAC23493.1; -. BC001395; AAH01395.1; -. BC032812; AAH32812.1; -.
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339 AA;
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SEQUENCE
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EMBL;
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11;
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                                                                                         222 VPSNKDVTS--LDWNSEGTLLATGSYDGFARIWTKDGN---LASTLGQ-HKGPIFALKWN 275
                                                                                                                                                                                   276 KKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCK 335
                                                                                                                                                                                                                                                                          336 LGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDN----CVHDLQAHNK 392
                                                                                                                                                                                                                                                                                                          451 SPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGS---V 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NEQG--VACSGSDPSWKCI 244
                                                                                                                                11 VPAHPDSRCWFLAWNPAGTLLASCGGDRRIRIWGTEGDSWICKSVLSEGHQRTVRKVAWS 70
                                                                                                                                                                                                                                                                                                                                                                                            EIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW--DVDRGICIHTLTKHQEPVYSVAF
                                                                                                                                                                                                                            -----wkknoddfecvt-----
    Length 339;
Score 349; DB 1;
Pred. No. 4.2e-18;
3; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 DPSGORLASCSDDRTVRIWRQYLPG-----
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                          1 Similarity 30.4%; Pr
92, Conservative 43;
                                                                                                                                                                                                                                 71 PCGNYLASASFDATTCI --
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Job time: 9.66667 secs
    Query Match
Best Local Similarity
Matches 92, Conserv
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

Run on:

August 9, 2004, 16:39:47 ; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec

US-09-987-701-12 2731 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

genesedp1980s:\*
genesedp1990s:\*
genesedp2000s:\*
genesedp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* 1: qeneseqp1980s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. score and is

geneseqp2004s:\*

# SUMMARIES

	Description	S Aab95225 Human pro		Add14051 Human	0	4 Abp51424 Human MDD	ø	Abg21351	Aa004385	Abg21350 Novel	Abr52980	Abr53774	Ada13321	Aar85881	Abb59486	Abb62260	Aay79678 Drosog	4 Aab68284 Amino	•	4 Aab92844 Human pro	Abb97306 Novel	2 Aab68282	ო	9 Aag48119 Ara	0 Adb95040	
	ΩI	AAB95225	ABC07190	ADD14051	ABP41760	ABP51424	ABB60376	ABG21351	AAC04385	ABG21350	ABR52980	ABR53774	ADA13321	AAR85881	ABB59486	ABB62260	AAY79678	AAB68284	AAB68516	AAB92844	ABB97306	AAB68282	AAG14893	AAG48119	ADB9504(	
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AAG14894 ABJ26155 AAW55957 AAW5888	ADE59633 ADE59705 ADE59697	ADE59709 ADE83378 ADE59701	ADE59713 ADE57861 ABB99407	ADA21145 AAM93784 ABB99402	ABB10141 ABP66728 ABP73371 AAG05554
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#### ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                          Saito K,
, Otsuki
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A, Nagai K,
                                                          Human protein sequence SEQ ID NO:17352.
              AAB95225 standard; protein; 514 AA
                                                                                                                                                                                                         Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                      27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-WAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                99JP-00248036.
                                                                                                                                 28-JUL-2000; 2000EP-00116126.
                                           (first entry)
                                                                                                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                29-JUL-1999;
                                                                                       Homo sapiens.
                                                                                                     EP1074617-A2.
                                           26-JUN-2001
                                                                                                                    07-FEB-2001.
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Ishii S,
                             AAB95225;
RESULT 1
AAB95225
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WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

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sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises at 3'-end sequence, where the chief sequence, and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are also useful for the AHH3632 to AAHH3632 represent human amino acid sequences; and AAHH3629 to AAHH3632 represent oligonucleotides, all of which are used in the exemplification of the
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Pred. No. 2.5e-245
                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                             98.5%;
98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                          Sequence 514 AA;
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RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                    RGTGGI FEVCWNAAGDKVGASASDGSVCVLDLRK
                                                                                                                                                                                                     Human p53 modifying protein, SEQ ID 150.
                                                                                                                           ABO07190 standard; protein; 514
                                                                                                                                                                             13-AUG-2003 (first entry)
          421
                                   481
                                                            481
                                                                                                                                                   ABO07190;
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The invention relates to identifying (M1) a candidate p53 pathway condulating agent, by contacting an assay system comprising a purified HW modulating agent, by contacting an assay system comprising a purified HM polyapetide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent, the system provides a reference contacting a cell defecting a test agent, the system provides a reference contacting a cell defecting a test agent, the system ordinate activity of the assay system. The specifically binds to a HM polypeptide comprising and manualian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic cacid) and diagnosing (M4) a disease in a patient (comprising contacting the sample with a probe for HM contacting the sample with a probe for HM comprision indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 * expression level. Contacting the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 * expression level. Contacting the p53 pathway of a cell the proposition of the cell, so that the cell undergoes normal contacting the p53 pathway of a cell, thus restoring the p53 pathway of a cell undergoes normal p53 pathway of a cell undergoes normal p53 pathway work as angiogenic, appoint or cell proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, approached the mann of a pathway modifying modification discorder in the p53 pathway such as angiogenic, and pathway modifying modification and p53 pathway modified th
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                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                          Funke RP;
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98.6%; Pred. No. 4.7e-245;
ive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 458-459; 678pp; English.
                                                                                                                                                                                                                                                                                                          Belvin M,
                                                                                                                                                                     05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                             03-JUN-2002; 2002WO-US017382.
                                                                                                                                                                                                                                                                                                       Friedman L, Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway in Drosophila.
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                                       WO200299122-A1.
Homo sapiens.
                                                                                   12-DEC-2002
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The present invention describes a predictor set comprising a plurality of the present invention describes whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase protein tyrosine kinase activity or members of the protein tyrosine kinase protein pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of determining whether the cells comprising obtaining a sample of cells, correlating the expression of the markers to the compound's ability to modulate the activity of the Cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels
                                                                                                                                                                              420
                                                                                                                                                                                                                                                                        DSTVRLWDVDRGICIHTLIKKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY 480
                                                                                                                                            360
                                                                     ATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKQNFILSAGVDKTTIIWDAHTGEA 300
                                                                                                                                     KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDPT
SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                              GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                                                                GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                   ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                         KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                                                                                                                                  DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase pathway; protein tyrosine kinase, cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides and polypeptides for predicting the activity of sounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                                                                                                       RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                                       RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human src biomarker polypeptide SEQ ID NO:240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD14051 standard; protein; 577
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correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polymuclectides and polypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polymuclectides or polypeptides, and selecting polymuclectides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polymuclectides and polypeptides are useful in predicting the polymuclectides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining disease sentivity in patients to allow the development of individualized sentity in patients to allow the development of individualized cancer) based on patient response at a molecular level. The present cancer is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NOOGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ATAATTTSAGVSHQNPSKNREATVNGEENRAHSV-NNHAKPMEIDGEVEIPSSKATVLRG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 HESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRRCIREGGHDVPSNKD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VISLDWNINGTILATGSYDGFARIWTEDGNLASTLGQHKGPIFALKWNRKGNYILSAGVD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQG 347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HESEVEICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTOLVLÄHCIREGGODVPSNKD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITIIMDAHTGEAKQQFPFHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 MSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPAALISILQKGLQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPNANLMLASASFDSTVRLWDVDRG1C1HTLTXHQEPVYSVAFSPDGRYLASGSFDKCVH
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                                                                                                                                                                                                                                                                                                                                                                                                                     89.3%; Score 2439; DB 7;
86.0%; Pred. No. 2.1e-221;
ive 33; Mismatches 27;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Sequence 577 AA;
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DB Huma
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder;

Human ovarian antigen HNOKM38, SEQ ID NO:2892.

--NOOGSAKN 126

SLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAT

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infertility, pregnancy disorder, anovulation, polycystic ovary syndrome; PCOS, ovarian cyst, dysmenorrhoea; endocrine disorder; infection; infulamentory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastroincestinal disorder; urinary system disorder; drug screening; gene threapy; chromosome mapping; forenoic analysis; antibody preparation; cyclostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                    07-JUN-2001; 2001WO-US018569.
                                                                                                                                                     07-JUN-2000; 2000US-0209467P
                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                       Birse CE, Rosen CA;
                                                                                                                                                                                                       WPI; 2002-147878/19.
N-PSDB; ABQ54837.
                                                                                                 WO200200677-A1
                                                                                Homo sapiens.
                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                             diseases.
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABP54131-ABQ56305), and also encompasses polypeptides 90% identical and polypucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens. Or ovarian antigens and the use of ovarian antigens polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast of pregnancy, anovulation, polyovitic ovary syndrome, ovarian cysts, and dysmenorines of polyovitic ovary syndrome, ovarian cysts, and dysmenorines of polyovitic ovary syndrome, ovarian or present of pregnancy, anovulation, polyovitic ovary syndrome, ovarian cysts, and dysmenorines, endocrine disorders, infections (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders cand urninary system disorders. Ovarian antigen polypucleotides and polymucleotides may also be used in screening for compounds which enterty of the process of the polymucleotides may the process.
Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and theis polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 2892; 2922pp; English.
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4 95

36 GFSHSAFTFXIESHISQSNINGTLVPPAALISILQKGLQYVEAEISINEDGTVFDGRPIE GFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVEAEVSINEDGTLFDGRPIE

85.8%; Score 2342; DB 5; Length 542; 85.4%; Pred. No. 2.9e-212; .ive 32; Mismatches 28; Indels 14

85.4%; Fir

Matches 434; Conservative

20

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Similarity

Query Match Local

Sequence 542 AA;

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275 GFARIWTEDGNIASTLGQHKGPIFALKWNRKGNYILSAGVDKTTINDAHTGEAKQOFPF
                                                                                                                                                                                                                                            335 HSAPALDVDWQNNTTFASCSTDMCTHVCRLGCDRPVKTFQGHTNEVNAIKWDPSGMLLAS
                                                                                                                                                                                                                                                                                                          395 CSDDMTLKIWSWKQEVCIHDLQAHNKEIYTIKWSPTGPATSNPNSNIMLASASFDSTVRL
                                                                                                                       215 GSGDSTARIWNINENSNGGSTQLVLRRCIREGGHDVPSNKDVTSLDWNTNGTLLATGSYD
                                        GENTANGEENGAHT LANNHTDMMEVDGDVEI PSNKAVVLRGHESEVFI CAWNPVSDLLVS
                                                         156 REATVNGEENRAHSV-NNHAKPWEIDGEVEIPSSKATVLRGHESEVFICAWNPVSDLLAS
                                                                                                   GSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYD
                                                                                                                                                               247 GFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                            HSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                        367 CSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                                      455 WDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVHIMNTQSGNLVHSYRGIGGI
                                                                                                                                                                                                                                                                                                                                                   427 WDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGI
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06-SEP-2000; 2000US-0230595P.
06-SEP-2000; 2000US-0230597P.
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2000US-0229751P.
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2000US-0230505F.
2000US-0230514F.
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2000US-0230517P.
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06-SEP-2000; 2
06-SEP-2000; 2
06-SEP-2000; 2
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05-SEP-2000;
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KQQFFFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                                                                                                                                                                                                                                                           305 KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDFT 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                             245 ATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                            QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEI PSNKAVVLRGHESEVFICAWNPV
                                                      125 QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPV
                                                                                                                 SDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                           185 SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                     241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7920; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 7920.
                                                                                                                                                                                                                                                                                                                                                                               GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 391
                                                                                                                                                                                                                                                                                                                                                                                                             365 GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 395
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila;
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                                                                                                              181
                                                                                                                                                                                                                                                                                          301
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ABB60376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (1) selected from a polypeptide having a sequence selected from 24 sequences (ABP5121-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence in munospanic fragment of (1). (1) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound for specifically binds (1) or modulates the activity of (1), and for preparing a polyclonal or monoclonal antibody by hybridoma technology.

Nucleic acids (11) (ABQ7244-ABQ7200) encocing (1) are useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for expression of moder in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the composition of MDDT in a sample. A composition comprising (1), an a sample, for detecting (1), in a sample. A composition comprising (1), an a sample, for treating a disease or condition and for purifying (1) from a sample, for detecting (1), in a sample. A composition comprising (1) or a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
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                                                                                                                                                                                                                                                                                          Yap PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                     Liu TF,
                                                                                                                                                                                                                                                              Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS; Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Dahl CR, Momiyama MG, Bradley DL, Rohatgi SD, Harris B; Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
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Pred. No. 1.1e-182;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 578; 618pp; English.
2000US-0230598P.
2000US-0230599P.
2000US-0230610P.
                                                               2000US-0230865P.
2000US-0230988P.
2000US-0230989P.
                                                                                                                               07-SEP-2000; 2000US-0230951P.
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98.5%;
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                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
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                                                               06-SEP-2000; 2
06-SEP-2000; 2
06-SEP-2000; 2
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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Best Local Simi
Matches 385;
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from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                            69.8%; Score 1906.5;
                                                                                                                  Query Match
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31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                   2001-639362/73
                                     Drmanac RT, Liu C,
                      (HYSE-) HYSEQ INC
                                                            N-PSDB; AAS85538
                                                                                                                                                                                                                                                                                                  Sequence 584 AA;
                                                                                                  biodiversity.
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                                EVEWSVGEDGEV - ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN
                                                                                   ------QQHAAAAAAAAATNQQGSAKNGENT
                                                                                                 119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDQSASEVDSSGNAANNAGGTYAGNNG
                                                                                                                               AGGNOASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS
                                                                                                                                                       | | | TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ
                                                                                                                                                                                                          FICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                         WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII
                                                                                                                                                                                                                                                  WDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                                                                              NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNAN
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                                                                                                                                                                            ------MEVDGDVEIPSNKAVVLRGHESEV
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         Indels 191;
                                                                                                                                                                                                                                                                                                                                                                       TGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                     EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ--
 Pred. No. 7.2e-171;
9; Mismatches 77;
                                                                                                                                               ----AHTIANNHTDM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #21342
                                                                                    ---QAYRDKLA-
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         49;
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 54.8%;
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         Matches 385; Conservative
  Best Local Similarity
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primeras, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and oaid sequences. ABG00010-ABG30377 represent novel human diagnostic mainto acid sequences. ABG00010-ABG30377 represent novel human diagnostic parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the widences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 LEVKGFSHSAFTFGIESHISQSNINGTLVPPSALISILQKGLQYVEAEISINKDGTVFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 KNREATVNGEENGAHEI-NNHSKPMEIDGDVEIPPNKATVLRGHESEVFICAMNPVSDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 VSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPVSDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 PFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT--------
                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 RPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1891.5; DB 4;
Pred. No. 1.4e-169;
4; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 51710; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDGFARIWTE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.3%;
Tang YT;
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Best Local Similarity 64.69
Matches 368; Conservative
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VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNK 392

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1 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL 60
                                                              121 VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNK
                                                                                                                                                                                          393 ELYTIKWSPTGPGTNNPNANLMLASAS 419
                                        273
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                                                                                                                                                                                                                                                                                    RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA0013410) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polynpeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, itsue growth factor activity, haematopoiesis regulating activity, itsue growth factor activity, manunomodilatory activity and activity, insue growth factor activity, manunomodilatory activity and activity, insue growth factor activity, manunomodilatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                            480
                                                                                                                  547
                                          487
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopolesis; tissue growth factor, immunomodulatory, cancer, leukaemia; nervous system disorders; arthritis; inflammation.
                        GMLLASCSDDMTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTGPATSNPNSSIMLASASF
                                                                                                    DSTVRLWDVEQGVCTHTLMKHOEPVYSVAFSPDGKYLASGSFDKYVHIWNTQSGSLVHSY
    GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                              DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 18277; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.8%; Score 1142; DB 4; Length 208; larity 100.0%; Pred. No. 2.4e-99; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                        RGTGGIFEVCWNAAGDKVGASASDGSVCVL 510
                                                                                                                                                                                            OGTGGIFEVCWNARGDKVGASASDGSVCIL 577
                                                                                                                                                                                                                                                                                      AA004385 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 18277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and treating e.g. leukemia,
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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N-PSDB; AAI84316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001.
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                                                                                                                                                                                            548
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    361
                                          428
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                                                                                                                                                                                                                                                    RESULT 8
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence to set in the interest and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutations
                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 51709; 103pp; English.
181 BIYTIKWSPTGPGTNNPNANLMLASAS 207
                                                                                                                                                                                                                              Novel human diagnostic protein #21341.
                                                                                                           Ä
                                                                                                           ABG21350 standard; protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS85537
                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT,
                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                   ABG21350;
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Similarity

Best Local Sim: Matches 207;

213 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL 272

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16;

DB 6; Length 535;

59 9

109 116

228 223 288 343

163

Matches

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117 ATNOQGSAKNGENTANGEENGAHTIANNHTDMM-EVDGDVEIPSNKAVVLRGHESEVFIC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 GQKYAVAFMDGQVNVYDLKKINSKSRSLYGNRDGILNPLPIPLYASYQSSQDNDYIFDLS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                  344 YQITEKIPIGKLIGHHGPISVLEFNDINKLLLSASDDGTLRIWHGGNGNSQNCFYGHSQS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRYLASGSFDKCVHIW-----NTQTGAL------VHSYRGTGGIFEVC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTIIWDAHTGEAKQOFPF-------HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 IVSASWV------GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVPIFAGRISQD 453
                                                                                                                                                                60 VEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAA
                                                                                                                                                                                        110 ETNSE-SNKAGEDGASTVERETQEDDTNSIDSSDDLDGFVKI--LKEIV---KLDNIVSS
                                                                                                                                                                                                                                                                                                                                                        164 TWNPLDESILAYGEKMSVARLARIVETDQEGKKYWKLTIIAELRHPFALSASSGKTTNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 VTILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV
                                                                                                       176 AWNPVSD-LLVSGSGDSTARIWNLSENSTSGPTQ-----LVLRHCIREGGQDVPSNKDV
                                                                                                                                                                                                                                                                                                                                                                                                            TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDK
                                                                                1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNIN-GALVPPAALISIIQKGLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiprotein complex; eukaryote; drug target; diagnosis
18.3%; Score 498.5; DB 6; 25.4%; Pred. No. 8.7e-38; ive 101; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNAAGDKVGA--SASDGSVCVL 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequence #SEQ ID 2413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2001; 2001EP-00111774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-) CELLZOME AG.
                     Similarity
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                       Local Sim
es 143;
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    Query Match
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                     Best Loca
Matches
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                                                                                                                                                                  309
                                                                                                                                                                                                                                                369
                                                                                                                                                                                                                                                                          PALDVDWQNNMTFASCSTDMCIHVCRLGCDHPVKTFQGHTNEVNAIKWDPSGMLLAVCSD 120
                                                                                                                                                                                                         9
                                                                                                                                                                RIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSA
                                                                                                                                                                                                         RIWTENGNLAITLCQHKGPIFALKWNKKGNYVLSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                              PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated protein complexes useful for diagnosing a disease
                                                                                                                                                                                                                                                                                                                                DMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLA 416
                                                                                                                                                                                                                                                                                                                                               DMTLKIWSMKQEVCIHDLQAHNKEIYIIKWSPTGPATSNPNSNIMLA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 825; 17pp + Sequence Listing; English
                                                                                  Length 167
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kruse UD,
                                                                             30.2%; Score 824; DB 4; L
86.8%; Pred. No. 2.1e-69;
iive 13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grandi P, Krause R, K
z JD, Superti-Furga GD;
  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR52980 standard; protein; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2001; 2001EP-00111774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein sequence #SEQ ID 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                     Local Similarity 86.89
les 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-250078/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gavin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ACC61022
                                           Sequence 167 AA;
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Marzioch M,
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                                                                                  Query Match
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Kruse UD,

Bauer A, Gavin A, Grandi P, Krause R, K. Marzioch M, Schultz JD, Superti-Furga GD;

WPI; 2003-250078/25.

Sequence 535

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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR513903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a balt and isolating the set of protein explainable by using a protein as a balt and isolating the set of protein up to 30 distinct proteins. Protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note in sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                      New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
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                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Mismatches 167; Indels
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                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2413; 17pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.7%; Score 375.5; DB 6; 23.6%; Pred. No. 3.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    document is available on CD-ROM
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N-PSDB; ACC61816
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SEO ID NO:3 Human intracellular signalling molecule INTSIG-3, intracellular signalling molecule; INTSIG;

cell proliferative disorder, cancer; atherosclerosis; autoimmune disorder; inflammatory disorder; infection; neurological disorder; developmental disorder; endocrine disorder; cytostatic; antiatreriosclerotic; nootropic; neuroprotective; cerebroprotective; immunosuppressive; antiinflammatory; gene therapy.

sapiens. Homo WO2003031568-A2

17-APR-2003

16-AUG-2002; 2002WO-US026322

24-AUG-2001; 2001US-0314751P.
31-AUG-2001; 2001US-0316752P.
31-AUG-2001; 2001US-0316847P.
34-SEP-2001; 2001US-032188P.
28-SEP-2001; 2001US-0326390P.
12-OCT-2001; 2001US-0326390P. 17-AUG-2001;

(INCY-) INCYTE GENOMICS INC

12-APR-2002; 2002US-0372499P.

Swarnakar A, Tang YT, Griffin JA, Emerling BM; MG, Ramkumar J, Richardson TW, Becha SD, Lee EA; Mason PM, Baughn MR, Li JX, Duggan BM, Gietzen KJ; ML, Ison CH, Thangavelu K, Xu Y, Lee S; aque WW, Azimzai Y, Hafalia AJA, Ding L, Nguyen DB; W, Chawla NK, Marquis JP, Jackson JL, Tran UK; L, he Tran U Lu DAM, Swarnakar i e IJ, Yao MG, Ramki BA, Lehr-Mason PM, Sprague WW, Luo W, Cha Yue n,
Forsythe IJ, ic.
Warren BA, Lehr-Mason ,
of. Borowsky ML, Honchell CD, Yue H,

2003-393436/37. N-PSDB; ADA13366

New human intracellular signaling molecules (INTSIG)), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, c infections

Claim 1; Page 225-226; 367pp; English.

The invention relates to 45 human intracellular signalling molecules (INTSIG), INTSIG-45, and the cDNAs encoding them (ADA13319-ADA13408). The invention also encomprissing an INTSIG nocletc acid sequence the recombinant preparation of a INTSIG; an antibody against a INTSIG; methods of detection of INTSIG proteins or nucleic acids; a micro-array containing INTSIG acids; methods of screening compositions computation of INTSIG proteins or nucleic acids; a micro-array containing INTSIG acids; to receive a composition composition acids; an arranged for their ability to modulate INTSIG activity or expression; and pharmaceutical compositions comprising an INTSIG protein, nucleic acids or preventing a variety of disorders, including cell proliferative disorders (e.g., cancer or atherosclerosis); autoimmune/inflammatory disorders (e.g., cancer or atherosclerosis); autoimmune/inflammatory disorders (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple cylematosis, osteoarthritis, rheumatoid arthritis, or systemic lupus erythematosus); neurological disorders (e.g., epilapsy, stroke, allergies, anaemia, asthma, disparsing, creating or anaemia, asthma, bronchitis, or systemic lupus erythematoral disorders (e.g., epilapsy, stroke, allergies, anaemia, asthma, asthma, pronchitis, or systemic lupus erythematoral disorders (e.g., epilapsy, stroke, allergies, anaemia, or parkinson's disease, allergies, anaemia, asthma, pronchitis, or systemic lupus disorders (e.g., disorders of the hypothalamus or pituitary gland or diabetes); reproductive disorders, or vesicle-trafficking disorders (e.g., cystic fibrosis or hypercholesteroleemia). The present sequence represents an INTSIG protein of the invention. disorders (e.g., epilepsy, stroke, Alzheimer's disease, dementia, or Parkinson's disease); developmental disorders (e.g., achondroplastic dwarfism, Cushing's disease, hypothyroidism or hydrocephalus); endoor protozoan or helminthic infections; neurological dwarfism, Cushing's disease, fungal, parasitic,

Sequence 414 AA

ADA13321 standard; protein; 414 AA

entry)

(first

06-NOV-2003 ADA13321;

ADA13321 ID ADA1 XX AC ADA1 XX DT 06-N

Matches

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Best Local Similarity 23.64
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                               254 NILIGHCAEISSASFNW-----DCSLILIGSMDKTCKLWDAINGKCVATLIGHDDEIL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins AAR85851-92 are protein which contain at least one WD-40 (also called beta-transducing homologous) amino acid repeat motifs. The WD-40 regions are involved in protein-protein interactions between proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
                                                                                                                                                                                             | ::|| | ::|:| :| ::|::| DKIATGSFDKTCKLWSVETGK-----CYHTFR-----GHTAEIVCLSFNPQSTLVA
                                                                                                                                                                                                                                                            TGSMDTTAKLWDIQNGEELTLRGHSAEIISLSFNTSGDRIITGSFDHTVVVWDADTGRKV
                                                                  --HAAAAAAAATNQQGSA-KNGE--
                                                                                           LLTASRTEQVKLLIÓRLOEKLGÓNSNHTFYLFKVLKAHILPLTNVÁLNKSGSCFITGSYD
                                                                                                                     ----NTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESBVFICAW-NPVS
                                                                                                                                                  ---TLEGHRNVVYAIAFNNPYG
                                                                                                                                                                            DLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNXDVTSLDWNSEGTLLA
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    which alter tinteracts with

                                     85;
           Length 414;
                                       Indels
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             Score 374.5; DB 6;
Pred. No. 3.2e-26;
; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                  LIDAVMPDVVQTRQQAYRDKLAQQ-
    13.7%; Scor.
26.7%; Pred
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                           Similarity
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                                     111;
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              Query Match
Best Local
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RESULT 13

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21;
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involved in intracellular signalling. An example of such an interaction is between protein kinase C and receptors of activated protein kinase (RACK), esp. RACK-1 (RAR85850). Proteins AAR85851-82 were isolated based on homology with beta-transducin, whereas proteins AAR85882-92 were isolated based on homology with the WD-40 consensus sequence (AAR85893). The proteins were used to construct the poptides AAR84928-R85063 and AAR85786-R85842. The peptides can be used to identify target proteins proteins involved in protein-protein interaction and to screen for drugs that will affect protein interaction involving WD-40 domains
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developmental biology; cell signalling; insecticide;

(first entry)

M Myers

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 LLVSGSGDSTARIWNLS----ENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 DEVNFLVYRYLQESGFSHSAFTFGIESHIS---QSNINGALVPPAALISIIQKGLQYVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                   invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 365; DB 4; Length 411;
22.7%; Pred. No. 2.5e-25;
ive 72; Mismatches 155; Indels 148;
Disclosure, SEQ ID NO 13572; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.7
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 KL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 411 AA;
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ABB62260 standard; protein; 411

ABB62260

Search completed: August 9, 2004, 16:45:35 Job time : 57 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 9, 2004, 16:41:43; Search time 13.3333 Seconds (without alignments) 3708.183 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-987-701-2 2726 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\* Database :

1: Pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable membrane	WD-40 repeat prote		w	40 repeat prot	O	10 repeat	WD-40 repeat prote		repeat	u	orc	beta transducin-li	hypothetical prote	WD-repeat protein	trp-asp repeat con	WD-40 repeat prote	WD-repeat protein	hypothetical prote	pro	건	hypothetical prote		hypothetical prote	WD-40 repeat-prote	LIS-1 protein - hu	probable WD-repeat	hypothetical prote	prot
SUMMARIES		60	o,	ıΩ		.,	3	0	9	2	6	7	6	9	ž.	0.	80	7	4	.7	06	,-I		2	2	2	3	4	7	ın
S	ΙD	548268	AC223	AI215	T1852	AF207	AI249	AE181	AE186	AD184	AG188	AC184	T4088	S7608	AH219	AB241	T4114	AG183	AH215	S1948	AF189	AE186	80535	S48052	AB220	AG237	836113	G8503	T0261	T3380
	DB	N	N	N	N	N	7	N	0	2	7	7	7	7	~	7	7	~	7	7	7	N	(1	(1	Ŋ	~	N	N	N	7
	Length	l W	52	25	1356	68	18	1227	70	71	934	1747	564	1693	676	1551	502	304	1189	515	265	677	437	410	559	786	409	333	323	473
o\-	Query		7.	۲.	16.9	9	9	16.1	Ġ.	'n	'n.	15.1	4.	4.	4	4.	m,	e,	m	m.	ش		•				12.4			
	Score		r	463.5	œ	•	Э Э	439	m	-		411.5				m					to.				44.	39.	337	m	3	•
	Result No.	н	7	m	4	S	9	7	ω	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

30 329 12.1 798 2 S34023 32 324 11.9 777 2 T00798 33 323.5 11.9 777 2 T41075 35 320.5 11.9 777 2 T41075 36 320.5 11.8 589 2 AG2400 37 319.5 11.7 606 2 T08180 310.5 11.4 704 2 S33263 309.5 11.4 704 2 S33263 309.5 11.4 357 2 TA2099 41 309 11.3 1091 2 S76414 42 305.5 11.2 317 2 T46032 44 304 11.2 605 2 T38932 45 300 11.0 701 2 T46032	g puipuid-xod ATAT	hypothetical prote	WD-repeat protein	hypothetical WD-re	hypothetical prote	WD-repeat protein	PF20 protein, micr	hypothetical prote	transcription init	WD-40 repeat prote	beta transducin-li	beta transducin-li	MET30 protein - ve	WD-40 repeat redul	probable sulfur me	hypothetical prote
326.5 326.5 323.5 323.5 323.5 320.5 310.5 310.5 310.5 310.5 310.5 310.5 310.5 310.5 310.5 309.5 30	S34023	T00798	AE2490	T41075	T19266	AG2400	T08180	T22703	833263	AI2099	T42045	S76414	849932	T46032	T38932	T16607
326.5 328.5 328.5 328.5 328.5 328.5 320.5 311.9 311.9 311.0 311.0 311.0 311.0 311.0 311.0 311.0 311.0 311.0 311.0 311.0 311.0 310.0	7	~	71	7	7	7	Ŋ	7	(1	7	7	7	7	7	N	7
329 326.25 326.25 320.21 310.5 310.5 309.5 309.5 309.5 309.5 309.5 309.5	798	787	342	777	376	589	909	579	704	357	1049	1191	640	317	605	701
329 326.5 326.5 320.5 310.5 310.5 310.5 309.5 309.5 309.5 309.5 309.5	2.1	2.0	1.9	1.9	1.8	1.8	1.7	1.6	1.4	1.4	1.3	1.3	1.3	1.2	1.2	1.0
	Н	_	-	-							-	Н	М	Н	-	Н
U U U U U U U U U U U U U U U U U	329	326.5	324	323.5	321	320.5	319.5	317.5	310.5	309.5	309	309	308	305.5	304	300
	30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1

S49268 probable membrane protein YBR103w - yeast (Saccharomyces cerevisiae) probable membrane protein YBR103w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Deteries: Saccharomyces cerevisiae C;Deteries: Saccharomyces cerevisiae C;Deteries: Saccharomyces cerevisiae C;Deteries: S48268; S45971; S44683 R;Mannhaupt, G.; Stucka, R.; Bhile, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994 A;Reference number: S48255; MUID:95208357; PMID:7900426 A;Reference number: S48255; MUID:95208357; PMID:7900426 A;Reference number: S48255; MUID:946645; PIDN:CAA55606.1; PID:9476059 A;Molecule type: DNA A;Molecule continuer: S45927 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45972 A;Accession: S45972 A;Accession: S45972 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971 A;Accession: S45971	A,Gene: SGD:SIF2 A,COSS-references: SGD:S0000307 A,COSS-references: SGD:S0000307 A,Map position: 2R C;Superfamily: unassigned WD repeat proteins; WD repeat homology C;Keywords: transmembrane protein F;355-388/Domain: WD repeat homology <wd1> F;357-429/Domain: WD repeat homology <wd2> F;341-450/Domain: WD repeat homology <wd2> F;341-450/Domain: transmembrane #status predicted <twm></twm></wd2></wd2></wd1>
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Gaps Query Match
18.4%; Score 502.5; DB 2; Length 535;
Best Local Similarity 24.9%; Pred. No. 3.3e-28;
Matches 142; Conservative 100; Mismatches 232; Indels 97;

15; 51 VNLVQRGILYTESELMVDSKGDISALNEHHLSEDFNLVQALQID------KEKFPEI 101 107 QAAAAAAAAAAQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166 102 SSEGRFTLETNSESNKAGEDGASTVERETQEDDTNSIDSSD--DLDGFVKI--LKEIV-- 155 50 ISIIQKGLOYVEAEVSINEDG----TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106 49 20 1 MSISSDEVNFLVYRYLQESGFSHSA------FTFGIKSHISQSNINGALVPPAAL 임 ò В ò g à

à qq

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beta transducin-like protein - Podospora anserina
C.Species: Podospora anserina
C.Dace: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T18521
R.Saupe, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
A.Pitle: A gene responsible for vegetative incompatibility in the fungus Podospora anseri
A.Reference number: Z18944; MUD:96009891; PMID:7557402
                                                                                                                                                                                                                                                                        Cyacession: A12155
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakanako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 206-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Ressidue: preliminary
A; Residues: 1-1258 eXUR>
A; Residues: 1-1258 eXUR>
A; Residues: 1-1258 eXUR>
A; Reperences: GB:BA000019; PIDN:BAB74499.1; PID:G17131893; GSPDB:GN00179
A; Reperences: atrain PCC 7120
C; Genetics:
A; Gene: a1r2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1152
                                                                                                                                                                                                                            strain PCC 7120
09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1391 TVRLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLWNISSGECLYTLHG 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
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A;Molecule type: DNA
A;Residues: 1.1356 <SAU>
A;Cross-references: EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 -----LRGHSNRVYSAIFSPNGEILATGSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1258;
                                                                                                                                                                       A12155
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
WD-repeat. Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp.
C;Date: 14-Dec_2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 463.5; DB 2;
31.8%; Pred. No. 6.7e-25;
iive 44; Mismatches 100;
                                                                      HINSVRSVAFSSDGLILASGSDDETIKLWDVK 1482
                                            -TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||| |: | ||| :| || 1227
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Matches 103;
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                                                                                     1451
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402239
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. pcC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC2239
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1183
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A;Residues: 1-1526 «KUR»
A;Cross-references: CB:BA000019; PIDN:BAB75165.1; PID:g17132599; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 IWNLSENS----TSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFAR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLASCSDDWTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVRLWDVDRGICIHTLIKHOEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                 444
                                                                                                                                                                                                                                                                                                                                                                                           324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 NSFYGHSQSIVSASWV------GDDKVISCSMDGSVRLWSLKQNTLIALSIVDGVP
                              QDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN
                                                    SSGKTTNQVTCLAMSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWNKDGT
                                                                                                              -HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                               325 CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                                               HDLQQHNXEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGAHTIANNHTDMMEVDGDVEIPPNKAV-VLRGHESEVFICAMNPVSDLLASGSGDSTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%; Score 479; DB 2; Length 15
29.8%; Pred. No. 6.8e-26;
Live 76; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                  445 VYSVAFSPDGRYLASGSFDKCVHIW-----NTQTGAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 GTGGIFEVCWNAAGDKVGA--SASDGSVCVL 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNDYIFDLSWNCAGNKISVAYSLQEGSVVAI 535
                                                                                                                  280 FILSAGVDKTTIIWDAHTGEAKQQFPF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALDVDWQSNNTF----
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Best Local Similarity 29.8%
Matches 117; Conservative
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WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120 c sp. PCC 7120 c;Species: Nostoc sp. PCC 7120 c sp. PCC 7120 c;Species: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 c;Accession: A12493 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 206-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anał A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                          :552 KTVKLMRSHDGHLLHTFSGHSNVVYSSSFSPDGRYIASASEDKTVKIWQIDGHLLTTLPQ 1611
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A,Status: preliminary
A,Molecule type: DNA
A,Rosidues: 1-1189 «KUR»
A,Experimental source: SB:BA000020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180
A,Experimental source: strain PCC 7120
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244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
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                                                                                                                                 .441 TLIGHDNEVNKVNFSPDGKTLASASRDNTVKLWNVSDGKFKKTLKGHTDEVFWVSFSPDG
                                                                                                                                                                               NLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFD
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                                                                                       OFFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
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                                                                                                                                                                                                                                                                                                                                                                      482 GTGGIFEVCWNAAGDKVGASASD 504
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Best Local Similarity
Matches 109; Conserv?
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A;Genome: plasmid
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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C,Accession: AF2071

R,Rammara, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shimte: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Reference number: AB1807; MUD:2159285; PMID:11759840

A,Status: preliminary

A,Status: preliminary

A,Molecule type: DAA
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----EVLAGNSGVYAVSFLHDGSIIATA 1381
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A;Residues: 1-1683 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73823.1; PID:g17131215; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                         320 ISTISVVEAEWNACTQT-----LEGHGSSVLSVAFSADGQRVASGSDDKTIKIWDT
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                                                                    Length 1356;
                                                                                                             Indels
                                                                                                                178;
                                                                 , DB 2;
1.3e-24;
                                                               16.9%; Score 460; DB 27.9%; Pred. No. 1.3e-iive 73; Mismatches
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Best Local Similarity
Matches 109; Conserv
                                                                                          Similarity
A;Gene: het-el
A;Introns: 761/3
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Matches
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30.8%;
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Best Local Similarity 30.8%
Matches 119; Conservative
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AE1866
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1866
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res: 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                         AE1810
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1810
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922 YTIGLWNLKTGECHPLRGHQGRIRSVAFHPDGKILASGSADNTIKLWDISDTNHSKYIRT 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                  862 WAIAFSPDGRTLISCSDDQTARLWDVITGNSLNILRGYTRDVYSVAFSPDSQILASGRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                151 VDGDVEI----PPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSE----NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682 LSKNINKVYSVAFSPDGRILASASQDQTIKLWDIATGNCQQTLIGHDDWVWSVTFSPVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNPILSAGVDKTTIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRPLLLASSSADQHIKLWDVATGKCLKTLKGHTREVHSVSFSPDGQTLASSGEDSTVRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAHIGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDG
                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 439; DB 2; Length 1227; 25.4%; Pred. No. 3.7e-23; ive 83; Mismatches 157; Indels 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -IGPGIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP-
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----WEADSNRVWAVA
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Matches 122;
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R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A.F. Res. 8, 205-213, 2001
A.F. Res. Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A.R. Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ILASASIDGTVKLW 1585
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A;Accession: AE1866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1708 KUIR>
A;Cross-references: GB:BA000019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179
A;Cross-references: strain PCC 7120
C;Genetics: A;Gene: all0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1322 NGETIGSASI------DATLKLWSPOGLILGTLKGHNSWVNSVSFSPDGRIFASGS 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 ARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule, type: DNA
A;Residues: 1-1711 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB77808.1; PID:g17135262; GSPDB:GN00179
A;Experimental source: strain PCC 7120
G;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SINEDGIL----FDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQQAAAAAAAAAAASQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVIRGHESEVFICAWNPV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 GDSTARIWNLSENSTSGSTQLVLRHCIREGGDDVPSNKDVTSLDWNSEGTLLATGSYDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APALDVDWQSNN-TFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGEENGAHTIANNHIDMMEVDGDVEIPPNKAVV---LRGHESEVFICAWNPVSDLLASGS
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                      Length 1708;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                  ; Score 437; DB 2; Li
; Pred. No. 8.1e-23;
69; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDDTTVKLWS-RDGQLLHTLKEHSRRVNGVAWSPDGQ---
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09 199 PROGLANTSWEATHLY	QY 227DUTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKG 278  1430 SQKSNVNSVSFPRDEGKTFASAGWDGNITIWQRE-TLAHSSLTIQKUQNIITTVSYSPDG 1488  QY 279 NFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASGSTDMCIHVCKLG 337  1489 KTIATAASADNTIKLWDSQTQQLKTTLTGHKDRITTLSFHPDNQTIASGSADKTIKIWRVN 1548  QY 338 QDRPIKTPGGHTNEVNAIKWDFACCSDDWTLKIWSMKQDNCVHDLQQHNKEIVTI 397  1549 DGQLLRTLTGHNDEVTSVNFSPDGQFLASGSTDNTVKIW-QTDGRLIKNITGHGLAIASV 1607  QY 398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQDEPVYSVAFSPDGFRY 457  1608 KFSPDSHTLASASWDNTIKLWQVTDGKLINNLNGHIDGVTSLSFSPDGFIL 1658
DD 1281 DGGTIVSAGADNIYKLASRNGTLL	231 ISSLVTGLILALGLAGVAMLOGOKARMSETKAISSSAESFLANALEF. 68 EDGTLFDGRPIESLSLIDA.VMPDVVQTRQQAYRDKLAQQQAAAAAAAAA 278 -DGLIASIRAGRRIKGTDGIDANTRTQITETLQQSINFVREKORLAEHDGMLESVSFSPD 119 SQQSSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVF-ICAW 337 SKPIATASRDKTVKINSLDGKKQLVVLREEKGEGFFNSVAF 178 NPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGQQDVPSNKD-VTSLDWN 1

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                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL031764; PIDN:CAA21113.1; GSPDB:GN00068; SPDB:SFCC1235.09
A;Experimental source: strain 972h-; cosmid c1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELEKHYVDNHSSNEEASKTSIDGE----SLVNENPCKLPPYLTVPHICETTLTKADST 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 NGFCEHNNSNDHQLKILQDKGSGSPSSPVMPFKDKIEKRDIDITMADESNVEKDPARPIA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 VYNSSPV----TEITEIKOVTFTGGEDIKSDFFKVIPTKHPVTCADWRPLLQENYHVYE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 SGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 YAFFSGVIEIYDSHGSQILSFHNNKGPVLSLKWSGTDTYLAAGSADGTITLFD----QLK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 LAVAS-NSIVSMYNAISLQQLAVFMRHTAPVSALSFSHNGRYLATGDTSGGVCINSCKTA 507
                                                                                                                         WD repeat protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T40883
R;Wood, V, Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the BMBL Data Library, September 1998
A;Reference number: Z21954
A;Reference number: Z21954
A;Reference number: Z21954
A;Reference number: Z21954
A;Reference number: L5564
A;Molecule type: DNA
A;Residues: 1-564 <WOO>
                         ASGSADNTIKLWNLPNATLLKTILGHPGKINTLAFSPDGKTLLSGGEDAGVMVMNL 1714
     512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNIN---GALVPPAALISIIQKGLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEAEV -----SINEDG--TLFDGRPIESLSLID-----AVMPDVVQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RQQAYRDKLAQQQAAAAAAAAAASQQGSAKNG-----ENTANGEENGAHTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 NNHTDMMEVDGDVEIPPNKAVVLRGHE---SEVF-----ICA-WNPVSD----LLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TGSYDGFARIWTXDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 Q-QFPFH--SAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTF-QGHTNEVNAIKW
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876086
beta transducin-like protein, 190K - Synechocystis sp. (strain PCC 6803)
 ASGS FDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 NLRISLLLTASSDTTVKLWSRGDAGAFECLH-VFSFSSPVNCIDW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 390.5; DB 2;
ilarity 24.5%; Pred. No. 3.7e-20;
Conservative 107; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 18/1; 273/3; 413/3
                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPCC1235.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 133; Conserv
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A; Residues: 1-1693 «KAN»
A; Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10064.1; PID:d1010711:
A; Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10064.1; PID:d10711:
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: unassigned WD repeat proteins; WD repeat homology «WD01»
F;1091-1084/Domain: WD repeat homology «WD01»
F;1092-1125/Domain: WD repeat homology «WD01»
                                                                                                                                                                                         R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: Nostoc 2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH3195
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI 397
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 RDKLAQQQAAAAAAAAAASQQGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Gaps
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A; Status: nucleic acid sequence not shown; translation not A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.3%; Score 388.5; DB 2;
Best Local Similarity 28.5%; Pred. No. 2.3e-19;
Matches 107; Conservative 52; Mismatches 138;
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F;1584-1617/Domain:
F;1625-1658/Domain:
                                                                                                                                                 C; Accession: S76086
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F;1174-1207/Domain:
F;1256-1289/Domain:
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RESULT 15
AB2410
WD_repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. Strain PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Accession: AB2410
C;Accession: AB2410
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C;Accession: AB2410
C;Accession: AB2410
C;Accession: AB2410
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2410
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                       A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Reference number: AB1807; MUD:21595285; PMID:11759840
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A;Accession: AH2195
A;Accession: DNA
A;Molecule type: DNA
A;Residues: 1-676 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74818.1; PID:g17132214; GSPDB:GN00179
C;Genetics:
A;Gene: alr3119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 VKVLNKLLETDIQRRYQSADEVMNDLIKQRSLLSRLKTTIPKSAIFSRSWSASTSLTAST 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAKNGENTANGEENGAHTIANNHIDNMEVDG-------DVEIPPNKAVVLRG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 TKKQAWKLINGRLK-QQLLINTMSALLGLVGVGHLQSLPQLITKFSEISTQP---YTLKG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGDDVPSNKD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTTIIWDAHIGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQ 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119;
                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 382.5; DB 2; Length 676; 23.6%; Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 FSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVEA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123; Conservative
205-213, 2001
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Matches 123; Conserv
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-----ATGSYDGFARIWTKDGNLASTLGOHKGPIFALKWNKKGNF 280

1053 AGDDHTARLWSFSGQQLVQFPGHQGTVWCISFSPDGKHIATAADDRIVRLWNLKGKLLVR 1112 

993 HEDTIWSANFSPDGKYIATASSDRTARLWNFSGQQLAKFQGHQGYVRSVSFSPDGKHIAT 1052

168

954 AWVRSVSFSRDGQYILIASDDCTAR------LWNLQG------KQLISLQG 992 HESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTS-----GSTQLVL-----RHCIR 216

108 AAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRG 167

903 ALMSAMRSG----KALQALVKDGRSLAKYPATSPLLALQTILDNIQERNQ-----FQGHQ

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48 ALISIIQKGLQYVEAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQ 107

; Score 382; DB 2; Length 1551; ; Pred. No. 6.1e-19; 94; Mismatches 193; Indels 130;

14.0%; 22.6%;

Conservative

Query Match Best Local Similarity Matches 122; Conserv

ILSAGVDKTTIIWDAHTGBAKQQFPFHSAPALDVDWQSNNTF-ASCSTDMCIHVCKLGQD

281

241

340 1232 400

RPIKTFOGHTNEVNAIKWDPIGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKW 399

Q-FSAFQGHQSTVRSVDFSPDGQKVVTAADDRTVRLWNIKGEELLQFL-GHRGKVWSVSF

SPIGPGINNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLAS

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9, 2004, 16:48:48
completed: August
 Search cor
Job time
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1340 ASSDLTTRLWSLDGQELMQFKGHDKWVRYVSFSCNGQHIATAADDCTARLWNLAGRQVG 1398

460 GSFDKCVHIWNTQTGALV-----

-----HSYRGIGGIFEVCWNAAGDKVG 499

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August 9, 2004, 16:41:13 ; Search time 34.6667 Seconds (without alignments) 4678.164 Million cell updates/sec
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1 MSISSDEVNFLVYRYLQESG.....GDKVGASASDGSVCVLDLRK 514
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Gen Core version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O8bhis musculu	mus	mus			OSbmm 0mm OSbmm	O86uv2 homo sapien	OSCOAL MUS MUSCULLI	09xzkl drosophila	O9fn19 arabidopsis	OBved3 mus musculu	095ri9 drosophila	O8x1p4 podospora a	Osxlus podospora a		Q8x1p2 podospora a
		!							-								
SUMMARIES	ID	Q8BHJS	Q8CBG4	Q9EQD4	67SZM9	OBBYO4	OBBMMO	QBGUY2	OSCOAL	QSXZK1	O9FN19	Q8VEG3	Q95RJ9	Q8X1P4	08X1P5	O8X1P3	Q8X1P2
	DB	1	11	11	13	11	11	4	11	വ	10	11	2	m	m	m	m
	Query Match Length DB	514	514	514	519	527	527	577	412	700	613	201	524	1356	1356	1356	1376
ф	Query	98.7	98.6	98.6	97.0	91.1	91.0	89.4	72.4	69.8	50.9	40.2	33.9	17.5	17.4	17.3	16.5
	Score	2691	. 2688	2687	2644.5	2484.5	2480.5	2437	1972.5	1904.5	1387	1096	923.5	477	474	472	449
	Result No.	н	N	m	4	ഹ	9	7	Φ	መ	10	11	12	13	14	15	16

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Q8YL09	08Z0R1	Q8YZI2	Q8Z019	Q8YZ23	Q8Z0Z0	074845	Q8YSG6	Q8YMU3	Q8N136	Q8TMX4	074855	Q9VPR¥	Q8T4A2	Q8N776	Q9D4T2	Q8Z054	QSYTD1	869960	Q9XBD8	096995	Q803D2	093531	Q7ZXK9	Q8YZ16	08080	Q98HK1	Q90ZL4	Q9DCZ7
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439.5	439	437	414	412.5	411.5	390.5	382.5	m	376	372	371.5	370.5	370.5	370	368.5	368.5	368.5	368	364	362.5	361.5	361	361	360	359	358.5	52	354
17	18	13	20	21	22	23	24	25	56	27	28,	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT Q8BHJ5 ID Q	1 8BHJ5 8BHJ5;	PRELIMINARY;	PRT;	514 AA.	
占	2003 (		Created)	1000	
H		250		sequence update/ annotation update/	
DE	prc			4	
N S	IRAL OR 8030499H02RIK.	HOZRIK.			
SO	Mus musculus (Mouse)	ouse).			
ე <u>წ</u>	Eukaryota; Metazoa; Chordata;	zoa; Chordata;		Craniata, Vertebrata, Euteleostomi,	
38	NCBI TaxID=10090:	ช	SCINFOR	sciurognatni; Muridae; Murinae; Mus.	
N.	[1]				
RP	SEQUENCE FROM N.A.	Α.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;	; TISSUE=Testi	· m		
ZX ZX	MEDLINE=22354683; PubMed=12466851	3; PubMed=1246	5851;		
RA	The FANTOM Consortium,	ortium,			
RA		RIKEN Genome Exploration Research	Research	Group Phase I & II Team:	
RT	"Analysis of the	of the mouse transcriptome based	riptome	pased on functional	
RT		gth cDNAs.";			
RL	Nature 420:563-5	420:563-573 (2002).			
DR	EMBL; AK029595;	BAC26526.1; -			
DR	EMBL; AK033347; BAC28241.	BAC28241.1; -			
DR	PIR; PT0651; PT0651.	1651.			
DR.	MGD; MGI:2441730; Iral.	); Iral.			
DR	InterPro; IPR006594; LisH	5594; LisH.			
DR	ro;	IPR001680; WD40.			
DR		4D40; 8.			
DR		PR00320; GPROTEINBRPT			
DR	ProDom; PD000018; WD40;	3; WD40; 3.			
DR	SM00667;	LisH; 1.			
DR	M00320;	WD40; 8.			
DR	PS50896	ij			
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DR	PS502	3	REGION;	η.	
SO	SEQUENCE 514 A	AA; 55661 MW;	13BEC1	13BECIC2C7F8BF14 CRC64;	

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STRAIN-CSTEL/61; TISSUE=Cerebellum,

MEDLINE=22154683; PubMed=12466851;

The FANTON Consortium,

The RAKEN Genome Exploration Research Group Phase I & II Team,

The RAKEN Genome Exploration Research Group Phase I & II Team,

Thanlysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

In Nature 420:563-573(2002)

R BMBL, AK036064; BAC29294.1; -.

R BMBL, AK036064; BAC29294.1; -.

R DATH PF00400; WD40.

R InterPro; IPR001689; M240.

R PF100M; PD0000189; WD40.

R PRINTS; PR00320; GPROTEINBRPT.

R PRINTS; RN00667; Lish; M240.

R SMART; SM00667; Lish; B.

R SMART; SM0067; Lish; B.
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                                                                    Indels 0; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
   98.7%; Score 2691; DB 11; Length 514; 98.6%; Pred. No. 6.2e-179; ive 2; Mismatches 5; Indels 0
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Last annotation update)
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Query Match
Best Local Similarity 98.69
Matches 507; Conservative
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Zhany X., Dormady S., Basch R.;
Zhany X., Dormady S., Easch R.;
Identification of four human cDNAs that are differentially expressed
by early hematopoietic progenitors.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, APZ68195; AAG44738 1;
InterPro; IPR006594; LisH.
InterPro; IPR001659, WD40.
Pfem; PP00400; WD40; 8.
PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                         0; Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                            98.6%; Score 2688; DB 11; Length 514; 98.4%; Pred. No. 1e-178; trive 3; Mismatches 5; Indels 0;
PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
SEQUENCE 514 AA; $5689 MW; 133ED3753A725029 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 98.4%
Matches 506; Conservative
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor co-repressor complex subunit TBLRI.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                          .;
                                                                                                                                               514;
                                                                                                                                         Query Match
98.6%; Score 2687; DB 11; Length
Best Local Similarity 98.4%; Pred. No. 1.2e-178;
Matches 506; Conservative 2; Mismatches 6; Indels
                                                                                                               514 AA; 55689 MW; 6A72CE68A40C141F CRC64;
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             SMART; SM00667; LisH; 1.
SMART; SM00320; WD40; 8.
PROSITE; PS0086; LISH; 1.
PROSITE; PS00678; WD REPEATS_1; 4.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD REPEATS_2; 6.
PROSITE; PS50294; WD REPEATS_REGION; 1.
SEQUENCE 514 AA; 55689 WW; 6A72CE68A4(
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PD000018; WD40; 3.
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NCBI_TaxID=8355;
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                                                                                                                                                               1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALAPPAALISIIQKGLQYV
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STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                       519;
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                                                                     DB 13; Length
                                                                  Score 2644.5; DB 13; Lengt
Pred. No. 1.1e-175;
4; Mismatches 10; Indels
                                 5E998EDC8C892296 CRC64;
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                                 519 AA; 56043 MW;
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Transducin (Tbllx protein).
EMBL; AY225088; AAP20646.1;
                                                                                                     Conservative
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tes 500; Conserv
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              Receptor.
SEQUENCE
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                                                                  Query Match
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                                                                                    Best Loc
Matches
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DKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQ 346
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pituitary;
STRAIN=223546683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK030547; BAC27015.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                    514
                                                                                                                                                          480 HIWNIQSGSLVHSYRGIGGIFEVCWNARGDKVGASASDGSVCVLDLRK 527
                                                                                                                    467 HIWNTOTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK
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91.0%; Score 2480.5; DB 11; Lengt
Best Local Similarity 87.7%; Pred. No. 2.8e-164;
Matches 463; Conservative 28; Mismatches 22; Indels
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ProDom; PD000018; WD40; 3.
BYART; SM00667; Lis8H; 1.
SWART; SM00220; WH09; 8.
PROSITE; PS500896; LISH; 1.
PROSITE; PS50082; WD_REPEATS_1; 4.
PROSITE; PS50084; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
SRQUENCE 527 AA; 56832 MW; 0466F764ABA25CB0 CRC64;
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Last annotation update)
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MGD; MGI-1336172; Tbllx.
InterPro; IPR00659; LisH.
Interpro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Q8BMM0
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               Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., As Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., & Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., & Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., & Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., & Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., & Pahelton B., Ketreman M., Madan A.M., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., & Rodriguez A.C., Carimwood J., Schmutz J., Myers R.M., Butterfield Y.S., & Jones S.J., Marra M.A.;

Mones S.J., Marra M.A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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PROSITE; PSC0966, MD REPEATS 1; 4.
PROSITE; PSC0621, WD REPEATS 2; 6.
PROSITE; PSC0294, WD REPEATS REGION; 1.
SEQUENCE 527 AA, 56802 NW; 146435A9C51DFDA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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MGD; MG1:1336172; Tbl1x.

InterPro; IPR006594; LisH.

InterPro; IPR001680; WD40.

PEAM; PF00400; WD40; 8.

PRINTS; PR00320; GPROTEINBEPT.

SMART; SM00667; LisH; 1.

SMART; SM00320; WD40; 8.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequences."
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Matches 464; Conserv
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1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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TBL1X.
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01-MAR-2003 (
01-OCT-2003 (
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A REDLINE=22388257; PubMed=12477932;

A Lausner R.D., Collins F.S., Wagner L., Shemenc C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wann J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley S., Malan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

"Medencation and initial analysis of more than 15,000 full-length human
                                         419
                                                                       466
                                                                                                  479
                           GHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGT
                                                                  NNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCV
                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                             HIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                               480 HIWNTQSGSLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 527
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC052304; AAHS2304.1; -.
R InterPro; IPR001680; WD40.
R InterPro; IPR001680; WD40.
R PRINTS; PR00202; QPROTEIRBRPT.
R PRINTS; PR00302; QPROTEIRBRPT.
R SMART; SM00667; Lish; 1.
R SMART; SM00667; Lish; 1.
R SMART; SM0022; WD40; 8.
R PROSITE; PS00996; LISH; 1.
R RSOSTE; PS00996; LISH; 1.
R PROSITE; PS00996; LISH; 1.
R PROSITE; PS00992; WD REPEATS_2; 6.
R PROSITE; PS00994; WD REPEATS_2; 6.
R PROSITE; PS00994; WD REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                              TBL1X protein.
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Best Local Simi
Matches 453;
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Q86UY2
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Gaps

14;

Indels

Conservative

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C STRAIN=CSTBL/GY TISSUE=Medulla oblongata;

X MEDLINE=22354683; PubMed=12466851;

A The FANTON Consortium,

A the RANTON Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

B MGD; MGI-1336172; Tblix.

B RGD; MGI-1336172; Tblix.

B RGD; MGI-1336172; Tblix.

B RGD; MGI-13460; WD40; 8.

B RROSITE; PRO0018; WD REPERTS I; 4.

B RROSITE; PS00602; WD REPERTS I; 4.

B RROSITE; PS0062; WD REPERTS REGION; I.

B ROSITE; PS0062; WD REPERTS REGION; I.

B ROSITE; ROSOSIE; WD REPERTS REGION; I.

B ROSITE; ROSOSIE; WD REPERTS REGION; I.

B ROSITE; ROSOSIE; WD REPERTS REGION; I.

B ROSITE; ROSOSIE; WD REPERTS REGION; I.
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                                                                                                                                                                                                                                                                                                                                                                        HINEVNAIKWDPSGMLLASCSDDMTLKIWSMKQEVCIHDLQAHNKEIYTIKWSPTGPATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 MSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPAALISILQKGLQYV
                                                              BABVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAA---
                                                                                                                                                                                                                                                   HESEVFICAMNPVSDLLASGSGDSTARIMNLSENSTSGSTQLVLRHCIREGGQDVPSNKD
                                                                                                                                                                                                                                                                                 HESEVFICAMNPVSDLLASGSGDSTARIMULNENSNGGSTQLVLRHCIREGGHDVPSNKD
                                                                                                                                                                                                                                                                                                                                               VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                           KTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQG
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                                                                                                                                                       -----ASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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MEDINE=20196006; PubMed=10731132;

MEDINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,

April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

Beson K.Y., Benos P.V., Berman B.P. Bhandari D., Bolshakov S.,

Beson K.Y., Benos P.V., Berman B.P. Bhandari D., Bolshakov S.,

Burtis K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Heiman T.J., Wentland J.R., Houck J.,

Kalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

Kalmmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                  104 AQQQAAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAV 163
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                                                                                                                                                                                                           62 VLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVP 121
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                                                                                                                                                                                                                                                                                       122 SNKDVTSLDWNSDGTLLATGSYDGFARIWTEDGNLASTLGQHKGPIFALKWNKKGNYILS 181
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                                                                                                                                                                                                                                                                                                                                                                                   TPOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TFQCHTNEVNAIKMDPSCMLLASCSDDMTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 PGINNPNANLMLASASFDSTVRLWDVDRGICIHTLITKHQEPVYSVAFSPDGRYLASGSFD 463
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                                                                                                                        3 AATATSTAATTPAAAAQQNPPKNGEATVNGEENGAHAI-NNHSKPMEIDGDVEIPPSKAT
                                                                                                                                                                            164 VLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVP
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 KCVHIMNTQSGSLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 412
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DB 11; Length 412;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
72.4%; Score 1972.5; DB 11
87.6%; Pred. No. 4.4e-129;
cive 22; Mismatches 28;
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EBI OR CG4063.
Drosophila melanogaster (Fruit fly).
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    Query Match
Best Local Similarity 87.6
Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacaleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Roine B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RANG E.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Yao G., Yao G., Yao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., Xao G., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99234084; PubMed=10215623;
Dong X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W.,
2ipursky S.L.;
"ebi regulates epidermal growth factor receptor signaling pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTRAIN=Berkeley;
Celniker S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R.,
Celniker S.E., George R.A., Arcaina T.T., Baxter E., Blazej R.G.,
Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
Lomotan M.A., Mak J., Madada P., Moshrefi A.R., Moshrefi M., Nixon K.,
Pacleb J.M., Park S., Pfeiffer B., Punch E., Snir E., Twomey B.,
Wan K.H., Zhang R., Zieran L.L., Rubin G.M.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.8%; Pred. No. 4.9e-124;
Matches 385; Conservative 51; Mismatches 75; Indels 191; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; WD repeat. _____SEQUENCE 700 AA; 72387 MW; 28C6D8D07BB79FB7 CRC64;
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SWART; SM00667; LiseH; 1.

SWART; SM00320; WD40; 3.

PROSITE; PS50896; LISH; 1.

PROSITE; PS00037; WTS_LF1; 1.

PROSITE; PS00061; WD_REPEATS_1; 3.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50294; WD_REPEATS_2; 6.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-OCT-2003 (Markingland Mouse-ear cress).
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DNA Res. 4:401-414(1997).
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Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASTLGQHKGPIPALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQS
Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chang M., Chang C.H., Daled J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Maryven M., Palm C.G., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C. Wu H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 1387; DB 10; Length 613; 44.2%; Pred. No. 4.1e-88;
                                                                                                                                                                                                                                  Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB07645; BAB03017.1; --
EMBL; AR07645; BAA113228.1; --
EMBL; AY14332; AAA113228.1; --
InterPro; IPR006594; LisH.
InterPro; IPR006594; WD40.
Pfam; PF00400; WD40; B.
Prom; PR00320; GPROTEINBRPT.
Propom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat.
SEQUENCE 613 AA; 69772 MW; 04F40772311C0E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GDVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.2%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom, PD000018; WD40; 2.
SWART; SW00667; LisH; 1.
SMART; SW0020; WJ40; 8.
PROSITE; PS0096; MD LISH; 1.
PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS 2; 6.
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                                                                                                                                                                                        Ecker J.R.;
"Arabidopsis ORF clones.";
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les 272; Conserv
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us-09-987-701-2.rspt

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233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- MEVDGDVEIPPNKAVVLRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 GNNVQSGSSNAQSSAPSGTISSSTSGGAGTPAALVPWDIDENIEIPESKARVLRGHESEV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FICAMNPVSDLLASGSGDSTARIMNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 FICAMNPSRDLLASGSGDSTARIWDMSDANIN-SNQLVLRHCIQKGGAEVPSNKDVISLD 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDAHTGEAKQOFPFHSAPALDVDWQSNNTFASC------STDMCIHV-CK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDASTG-----PMHPAICL----SQCSSLGCGLADKPGLCLLQYGSADTCVPVGCK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 217; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ-----
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            524 AA; 52529 MW; 6C3D86110BA18D65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*4.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
33.9%; Score 923.5; DB 5;
Best Local Similarity 40.5%; Pred. No. 5.8e-56;
Matches 218; Conservative 39; Mismatches 64;
                                                         EMBL, AY061326, AAL28874.1; -.
FlyBase; FBGN0023444; ebi.
GO; GO:000074; P:regulation of cell cycle; IMP.
InterPro; IPR0016594; LisH.
InterPro; IPR001005; Myb DNA_binding.
InterPro; IPR001680; WD40.
                                                                                                                                                                         PERMY PRO0400; WD40; 3.

PRINTS; PR00320; GPROTEINBRPT.

PRODOM; PD0000018; W040; 1.

SMART; SW00667; LisH; 1.

SMART; SW00320; WD40; 3.

PROSITE; PS00037; WM81; 1.

PROSITE; PS00037; WM81; 1.

PROSITE; PS00037; WD REPEATS 1; 2.

PROSITE; PS00082; WD REPEATS 1; 2.

PROSITE; PS00082; WD REPEATS 2; 3.

PROSITE; PS00082; WD REPEATS 2; 3.
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                                                                                                                                                                                                                                                                                                                                                                              Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ANGEE----
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Q8X1P4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSCRGTGGIFEVCWNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 KIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGIFEVCWNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
Stapheton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapheton M., Drokstein V., Farfan D., Frise B., George R.
Champe M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.
Gonzalez M., Guarin H., Li P., Liao G., Miranda A.,
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BBI OR CG4063.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophiladee; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018512; AAH18512.1; -. InterPro; IPR001880; MD40. Pfam; PF00400; WD40; 4. PRINTS; PR00030; GPROTEINBRPT. Propon; PD00018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
201 AA; 22038 MW; 6B945F137B491818 CRC64;
                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to IRA1 protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.2%; Score 1096; DB 11; Best Local Similarity 99.0%; Pred. No. 1.5e-68; Matches 199; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 AA.
                                                                                                         201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00320; WD40; 4.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS50082; WD REPEATS 2; 3.
PROSITE; PS50294; WD REPEATS REGION; 1.
Repeat; WD repeat.
1
SEQUENCE 201 AA; 22038 MW; 6B945F13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                         PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
          598 AACFADNSVCVLDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                         PRELIMINARY;
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                                                                                                         08VEG3
                                                                RESULT 11
Q8VEG3
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Beta transducin-like protein HET-E2C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053 ----WVQSVAFSPDGQRVASGSNDHTIKIWDAASGTCTQTLEGHGDSVWSVAFSPDGQRV 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 -TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484
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                                                                                           Language B., Balhadere P., Begueret J., Turcq B.;

Beyagne B., Balhadere P., Begueret J., Turcq B.;

Tanew family of Word proteins implicated in vegetative family of Word proteins implicated in vegetative in compatibility; evidence for a major role of WD40 repeat domain in the specificity of het-e and het-d genes.";

Laubmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

REMEL, AF323583; AAL37299.1; ...

REMEL, AF323583; AAL37299.1; ...

REMEL, PRO00711; NACHT NTPASE.

REMEL, PRO0120; MA40.

REMEL, PRO120; GROCTEINBRPT.

REMINTS; PRO130; WA40; 10.

REMELS SM013020; WA40; 10.

REMELS SM013020; WA40; 10.

REMELS PROSITE; PS5083; WAERPEATS. 1; 10.

REMOSITE; PS5083; WAERPEATS. 1; 10.

REMOSITE; PS5084; WD_REPEATS. 2; 10.

REMOSITE; PS5094; WD_REPEATS. 2; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769 LIAIVRDGYRFALSYRMIIEKAPLQAYTSALVFAPTDSMIKKIFKKEEPGWISTISVVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEIPP-----NKAV----NKAV-----VLRGHESEVFICAWNPVSDLLASGSGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      889 VAFSPDGQRVASGSDDKTIKIMDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 ASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASPDSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 RLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 LISIIQKGLQYVEAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQA
     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                         Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora
NCBI TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.5%; Score 477; DB 3; Length 1356; 26.2%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1356 AA; 149702 MW; 33148AF4A7B82826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Mismatches
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SEQUENCE 1356 AA
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Matches 133;
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Last sequence update) Last annotation update)

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(TrEMBLrel. 20, TrEMBLrel. 20, (TrEMBLrel. 25,

01-MAR-2002 ( 01-MAR-2002 ( 01-OCT-2003 (

Q8X1P5; Q8X1P5

1356 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  995 DTASGTCTQTLEGHGNSVWSVAFSPDGQRVASGSDDKTIKIWDTASGTCTQTLEGHGGWV 1054
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                                                                                                                                                                                                                                                                                                                   Espagne E., Balhadere P., Begueret J., Turcq B.;
"A new family of WD40 proteins implicated in vegetative incompatibility; evidence for a major role of WD40 repeat domain in the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, RF202582; AAL37298.1; -.
InterPro; IPR00711; NACHT_NTPase.
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Podospora anserina.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 474; DB 3; Length 139; Pred. No. 4e-24; 86; Mismatches 222; Indels
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1356 AA; 149720 MW; 9A80777304B361D0 CRC64;
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Pfan, PPG5729; NACH7, 1.
Pfan, PPG0400; WD40; 1.
PRINTS; PRG0320; GPROTEINBRPT.
PROSIT; SMG0320; WA40; 10.
PROSITS; PS56083; NACH7, 1.
PROSITS; PS5062; WD_REPEATS_2; 10.
PROSITS; PS5062; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_3; 10.
PROSITS; PS5024; WD_REPEATS_3; 10.
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Matches 132; Conservative
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=5145
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Q8X1P3
ID Q8X1P3
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969 --SVWSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHGNSVWSVAFSPDGQRVAS 1026
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                                                                                                                                                                                                                                                                                                                            Les Bayene E., Balhadere P., Begueret J., Turcg B.;

Bayene E., Balhadere P., Begueret J., Turcg B.;

"A new family of WD40 proteins implicated in vegetative
incompatibility; evidence for a major role of WD40 repeat

"The specificity of het-e and het-d genes.";

"The specificity of het-e and het-d genes.";

"BMB1, AF32384; AAL3700.1; -.

"BMB1, AF32384; AAL3700.1; -.

"InterPro; IPR00111; NACHT_NTPase.

"InterPro; IPR001111; NACHT_NTPase.

"The Pro; IPR001111; NACHT_NTPase.

"The Pro; IPR00111;   NACHT_NTPASE.

"The Pro; IPR0011111; NACHT_NTPASE.

"The Pro; IPR00111111; NACHT_NTPASE.

"The Pro; IPR00111111; NACHT_NTPASE.

"The Pro; IPR0011111; NACHT_NTPASE.

"The Pro; IPR0011111; NACHT_NTPASE.

"The Pro; IPR00111111; NACHT_NTPASE.

"The Pro; IPR00111111; NACHT_NTPASE.

"The Pro; IPR00111111; NACHT_NTPASE.

"The Pro; IPR00111111;
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                                                                                                                                                                                     Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
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31.7%; Pred. No. 5.5e-24;
ive 59; Mismatches 154; Indels
01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*40.
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Best Local Similarity 31.7%
Matches 111; Conservative
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9, 2004, 16:39:47; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec
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Compugen Ltd.
GenCore version
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 sed Minimum DB Maximum DB

1586107

Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

geneseqp1980s:\*
geneseqp200s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003bs:\*
geneseqp2003bs:\* 29Jan04:\* A\_Geneseq Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ADE59693 ADE59705 ADE59697	ADE59709 ADE83378 ADE59701 ADE59713	ADE57861 AAR70002 ADE58488 ADE83492	ADE54233 AAR70005 ABB59486 AAY79678	AAW06085 AAW25018 AAR85868 ABB99407 ADA21145
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### ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                             Saito K, You Otsuki T;
                                                                                                                                                                                                                              Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                               Human protein sequence SEQ ID NO:17352.
               AAB95225 standard; protein; 514 AA
                                                                                                                                                            29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300233.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                              28-JUL-2000; 2000EP-00116126.
                                               (first entry)
                                                                                                                                                                                                              (HELI-) HELIX RES INST
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                                                                                                Homo sapiens.
                                                                                                              EP1074617-A2.
                                               26-JUN-2001
                                                                                                                               07-FEB-2001.
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Ishii S,
                                AAB95225
RESULT 1
        AAB95225
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Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

12-DEC-2002

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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at 3'-end sequence, where the combination of the 5'-end sequence is nucleotides and the combination of specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18472 represent human cDNA sequences; AAB2446 c AAB95893 represent human amino acid sequences; and AAH13629 to AAB413632 represent oligonucleotides, all of which are used in the exemplification of the
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91.5%; Score 2488; DB 4; Length 514;
Best Local Similarity 99.4%; Pred. No. 2.1e-224;
Matches 469; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                             present invention
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Human, p53 modifier, cytostatic, cancer, cytostatic, antiangiogenic, antiapoptotic, p53 pathway, breast cancer, colon cancer, kidney cancer, lung cancer, ovarian cancer, angiogenesis, cell cycle, apoptotic disorder, cell proliferation disorder.
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                                                                                                                                                                    ABO07190 standard; protein; 514 AA
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RESULT
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WO200299122-A1

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The invention relates to identifying (Mi) a candidate ps; pathway modulating agent, by contacting an assay system comprising a purified HW modulating agent, by contacting an assay system conditions, where but Drosophila) or nucleic acid with a test agent under conditions, where but Cor the presence of the test agent. The system provides a reference activity, and detecting a test agent. Diased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HW polypeptide comprising an HW amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway of a cell (comprising contacting the cell with an agent that specifically binds an HW polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising; (a) obtaining a biological sample of from the patient; (b) contacting the sample with a probe for HW expression, (c) comparison indicates a likelihood disease). (M1) is useful cor identifying modulators of the p53 pathway, a probe for HW expression for is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where disease or disease or disarder prognosis is related the patient of modulating the p53 pathway of a cell, thus restoring the p53 pathway such as angiogenese normal cor also useful for reating defects in the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, approttic or cell profileration disorders. The present sequence
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                                                                                                                                                                                                                                                                                                                                 Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGSAKNGENTANGEENGAHTIANNHTDMÆVDGDVBIPPNKAVVLRGHESEVFICAWNPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to identifying (M1) a candidate p53 pathway
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91.4%; Score 2485; DB 6;
Best Local Similarity 99.4%; Pred. No. 4e-224;
Matches 469; Conservative 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 458-459; 678pp; English
                                                                                    2001US-0296076P.
2001US-0328605P.
2002US-0357253P.
                                         2002WO-US017382
                                                                                                                                                                                                                            Friedman L, Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                            pathway in Drosophila.
                                                                                                                                                                                (EXEL-) EXELIXIS INC
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                                             03-JUN-2002;
                                                                                                               10-OCT-2001;
15-FEB-2002;
                                                                                       05-JUN-2001;
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The present invention describes a predictor set comprising a plurality of polymucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polymucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polymucleotides and
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 ATGSYDGFARIWTKDGNLASTLGQHKGP1FALKWNKKGNF1LSAGVDKTT11WDAHTGEA
                  KOOFPHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                  KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                       GNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                   GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides and polypeptides for predicting the activity of sounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                  DSTVRLWDVDRGICIHTLITKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                472
                                                                                                                                                                                                            DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human src biomarker polypeptide SEQ ID NO:240.
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                                                                                                                                                                                                                                                                                                                                   AA.
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                                                                                                                                                                                                                                                                                                                                   standard; protein; 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2003; 2003WO-US001981.
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase pathways.
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N-PSDB; ADD14646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 HESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 VTSLDWNTNGTLLATGSYDGFARIWTEDGNLASTLGGHKGPIFALKWNRKGNYILSAGVD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 KTTIIWDAHTGEAKQQFPFHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 HTNEVNAIKWDPSGMLLASCSDDMTLKIWSWKQEVCIHDLQAHNKEIYTIKWSPTGPATS 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD 287
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expression pattern of the microarray. The polynucleotides and polypeptides have cytostatic activities, and can be used in gene therapy. The polynucleotides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining and sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary, ovarian; breast, cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCGS; ovarian cyst; dysmenorinoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                        1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVH
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                           Length 577;
                                                                                                                                                                                                                                                    82.0%; Score 2229; DB 7; Length 5'85.4%; Pred. No. 5.5e-200;
ive 32; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody preparation; cytostatic; immunomouumae
antiinflammatory; gynaecclogical; reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ovarian antigen HNOKM38, SEQ ID NO:2892.
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85.4%; F.
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Matches 414; Conservative
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                                                                                                                                                                                                               Sequence 577 AA;
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a microarray of polynuclectides or polypeptides, and selecting polynuclectides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the

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(INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Human MDDT SEQ ID NO 446.
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06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polybrucleotides 93% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen corrections and host cells comprising human ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tunnurs of ovarian or breast origin, reproductive system disorders (e.g., inflating or preventing various ovary and/or breast-related disorders, inflating covarian cysts, and dysmenorthoea), endocrine disorders, inflating or preventing various, anovulation, polycystic ovary syndrome; ovarian cysts, and dysmenorthoea, endocrine disorders, inflating or congenital and acquired cancer, and used manually inflating ophoritis and various or vaginitis), immune disorders (e.g., congenital and acquired condeficiencies, autoimmune ophoritis, systemic lupus erythematosus), clood-related disorders (e.g., anaemia), cardiovascular disorders condulate ovarian antigen polypeptides and ophoritis and polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies claence data for this parent did not form part of the printed sequence represents a human ovarian antigen of the invention. Note: The specification, but was obtained in electronic format directly from MIPO contractly directly from WIPO contractly directly from wiponed and discorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAA.-------ASQQGSAKN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 GENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVEAEVSINEDGTLFDGRPIE
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78.4%; Score 2132; DB 5; Length 542;
Best Local Similarity 84.8%; Pred. No. 6.5e-191;
Matches 395; Conservative 31; Mismatches 26; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 2892; 2922pp; English
                                                                                                  07-JUN-2001; 2001WO-US018569
                                                                                                                              07-JUN-2000; 2000US-0209467P
                                                                                                                                                        (HUMA-) HUMAN GENOME SCI
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                                         WO200200677-A1.
               Homo sapiens.
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                                   215 GSGDSTARIWNINENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWNTNGTLLATGSYD
                                                                                                           GFARIWINDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                              GFARIWTEDGWLASTLGGHKGPIFALKWNRKGNYILSAGVDKTTIIWDAHTGBAKQQFPF
                                                                                                                                                                                                                       307 HSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                                CSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                               472
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2000US-0229749P
2000US-0229751P
2000US-0239751P
2000US-0230563P
2000US-0230565P
2000US-0230505P
2000US-0230505P
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2000US-0230518P.
2000US-0230519P.
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2000US-0230597P.
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2000US-0230988P.
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Flores V;
                                                                                Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
          Yap PE;
         Liu TF,
                Harris B;
, Panzer SR,
5, Lincoln SE, Altus CM, Dufour GE, Chalup MS; TL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu Shaniyama MG, Bradley DL, Rohatgi SD, Harris B; AM, Gerstin RH, Peralta CH, David MH, Panzer SI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                               14; Page 578; 618pp; English.
Jackson S, Lincoln SE,
Hillman JL, Jones AL,
Dahl CR, Momiyama MG,
Roseberry AM, Gerstin
                                                      WPI; 2002-527544/56
                                                                 N-PSDB; ABQ72641
                                     Daffo A,
                                                                                                                                Claim
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The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (1) selected from a polypeptide having a sequence selected from 254 sequences (ABP51211-ABP51464) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (1) or a biologically active or naturally occurring polypeptide comprising a sequence compound for effectiveness as an agonist or antagonist, for screening a compound for effectiveness as an agonist or antagonist, for screening a compound for preparing a polyclonal or monoclonal antibody by hybridoma technology.

The specifically binds (1) or modulates the activity of (1), and for consequence of the compound for effectiveness in altering expression of a target compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (1) in a sample, and for purifying (1) from a sample. Accordated with decreased or increased expression of functional MDDT. (1) or (11) are useful for diagnosing, treating a disease or condition associated with aberrant expression of MDDT, where the disorders are cirrhosis, hepatitis for diagnosing, treating or preventing disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, poliferative disorder such as arteriosclerosis or theumatoid arthritis. (11) are useful for creating sore, in somethic or entering a cutoimmune/inflammatore and an expression of functional moder and an entering arthritis. (11) are useful for creating sore, in some or condition of the property in a standard in a transpense or condition or animals or transgenic entering a transcenic expression of animals or preservent or such a transcent or a transcent or property in a transcent or a transcent or a trans germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic sednences

Sequence 395 AA;

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120
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                                                                                                                                                                                                                                                                                                                                                                                                  245 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA 304
                                                                            9
                                                                                                             64
                                                                                                  5 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                           SDLLASGSGDSTARIWLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                          1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                   EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAASQ
                                                                                                                                                                                                                           OGSAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPV
                                                                                                                                                                                                                                                         125 QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAMNPV
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                                       Gaps
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 Length 395;
                                       Indels
75.3%; Score 2047; DB 5; 99.5%; Pred. No. 3.8e-183; iive 1; Mismatches 1;
                                       Matches 389; Conservative
                   Local Similarity
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 Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) elementary production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics. Gorensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WHOO at the printed specification, but was obtained in electronic format directly from WHOO at the printed specification.
KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                   305 KÖÖFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 364
                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 584;
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                                                                                GNLLASCSDDMTLKIWSMKQDNCVHDLQQHN 391
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                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #21342.
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                                                                                                                                                                                                                               ABG21351 standard; protein; 584
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                        ASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGS
                                                                                                                                                                               YDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIWDAHTGEAKQQF
                                                                                                                                                                                                                                                    305 PPHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT------
                                                                                                                                                                                                                                                                                                                  368 KLTTMTEGKRLRPKTFCSDGGALLPPAGRRPHLLTGPDIFFKRLSALFQNEVNALKMDPS
                                                                                                                                                                                                                                                                                                                                         GNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
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                                                                             --AAASQQGSA
                                                                                                                      KNGENTANGEENGAHTIANNHTDMMEVDGDVEI PPNKAVVLRGHESEVFICAMNPVSDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 7920
                                                                           RPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAA
    Pred. No. 2.7e-152;
63.5%; Pred. Actiones
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2000US-00614150
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   Best Local Similarity 63.5
Matches 338, Conservative
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVEWSVGEDGEV--ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN 118
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                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS-137-ABB72072). The sequence data for this parent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QAYRDKLA------QQQAAAAAAAAAAQQGSAKNGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSPSSDEWNFLVYRYLQESGFLHSAYVFGIESHISQSNINGALVPPAALLIILQKGLLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDÖSASEVDSSGNAANNAGGTYAGNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FICAMNPSRDLIASGSGDSTARIWDMSDANTN-SNQLVLRHCIQKGGAEVPSNXDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNNVQSGSSNAQSSAPSGTISSSTSGGAGTPAALVPMDIDENIEIPESKARVLRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDAHIGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII
                                                                                                                                                                                                                                                                              63.1%; Score 1715.5; DB 4; Length 700; 52.9%; Pred. No. 1.3e-151; ive 49; Mismatches 71; Indels 191;
                              Disclosure; SEQ ID NO 7920; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AHTIANNHTDM-
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.98
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGEE----
                                                                                                                                                                                                                                                  Sequence 700 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.

30-MAR-2001; 2001WO-US008631.

WO200175067-A2

11-OCT-2001.

Homo sapiens

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS85537

(HYSE-) HYSEQ INC

Novel human diagnostic protein #21341.

(first entry)

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The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerical polymerical are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, immunomodulatory activities, activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, architis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                       Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 18277; 1399pp + Sequence Listing; English.
                 Human polypeptide SEQ ID NO 18277.
                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 208 AA;
                                                                                                                                                                                                   WO200164835-A2.
                                                                                                                                                             Homo sapiens.
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272
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                                                                                                 9
                                                                213 HCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGPARIWTKDGNLASTLGQHKGPIFAL
                                                                                                                                 273 KWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIH
                                                                                                                                                            61 KWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIH
                                                                                                                                                                                              VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNK
                                                                                                 HCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGGHKGPIFAL
                                  Gaps
                                  ..
Length 208;
                                  1; Indels
Score 1137; DB 4;
Pred. No. 4.3e-98;
0; Mismatches 1;
                                                                                                                                                                                                                                                            EIYTIKWSPTGPGTNNPNANLMLASAS 419
                                                                                                                                                                                                                                                                                  EIYTIKWSPTGPGTNNPNANLMLASAS
 41.8%;
                                  Matches 206; Conservative
Query Match
Best Local Similarity
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ABG21350 standard; protein; 167 AA

ABG21350,

ABG21350 ID ABG2 XX AC ABG2

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites apprehens to protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patient did not appear in the printed specification, but was obtained in electronic format directly from WINPO at the printed specification, but was obtained in electronic format directly from WINPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 RIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIWTENGNLAITLCQHKGPIFALKWNKKGNYVLSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PALDVDWQNNMTFASCSTDMCIHVCRLGCDHPVKTFQGHTNEVNAIKWDPSGMLLAVCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.1%; Score 819; DB 4; Length 167; 86.2%; Pred. No. 2.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 51709; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 167 AA;
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us-09-987-701-4.rag

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20 ODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human intracellular signaling molecules (INTSIG)), useful for
                                                  280 FILSAGVDKTTIIWDAHTGEAKQQFPF-----
                                                                                                                                                                                                                                                                                                                                               ADA13321 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0322188P.
2001US-0326390P.
2001US-0328952P.
2001US-0345468P.
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2001US-0314751P.
2001US-0316752P.
2001US-0316847P.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Warren BA, Len.
The Borowsky ML,
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14-SEP-2001;
28-SEP-2001;
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Honchell CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002;
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31-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC6610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .07 QAAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ISIIQKGLQYVEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTO-----LVLRHCIREGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FTFGIKSHISQSNINGALVPPAAL
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                                                                                                                                                                                                                                                                                                                          Kuester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 825; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.3%; Score 469; DB 6; Length 53
Best Local Similarity 25.8%; Pred. No. 1.1e-34;
Matches 140; Conservative 91; Mismatches 230; Indels
                                                                                                                                            Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                          Kruse UD,
                                                                                                                                                                                                                                                                                                                        Gavin A, Grandi P, Krause R, K
1, Schultz JD, Superti-Furga GD;
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                                        ABR52980 standard; protein; 535 AA.
                                                                                                                                                                                                                                                                      15-MAY-2001; 2001EP-00111774
                                                                                                                  Protein sequence #SEQ ID 825
                                                                                                                                                                                                                                               20-DEC-2001; 2001EP-00130253
                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-250078/25.
                                                                                                                                                                                                                                                                                                (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACC61022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 535 AA;
                                                                                                                                                                                            EP1258494-A1.
                                                                                         20-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 VYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQVLLNLG-RSICLYTLPHHLVVIP 503
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215 SSGKTTNQVTCLAMSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWNKDGT
                                                                                                             ----HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                                                                                                                                                                                                                                                              HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, intracellular signalling molecule, INTSIG, cell proliferative disorder; cancer, atherosclerosis, autoimmune disorder; inflammatory disorder, infection; neurological disorder; developmental disorder; endocrine disorder; cytostatic, antiatreriosclerotic, noctropic, neuroprotective; cerebroprotective; immunosuppressive, antiinflammatory; gene therapy.
                                                                                                                                                                                                                                                                      CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCFYGHSQSIVSASWV-----GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human intracellular signalling molecule INTSIG-3, SEQ ID NO:3
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The invention relates to 45 human intracellular signalling molecules (INNSIG), INTSIG-1 to INTSIG-45, and the cDNAs encoding them (ADA13319-CC ADA13408). The invention also encompasses expression constructs, host cells and transgenic organisms comprising an INTSIG nucleic acid sequence; the recombinant preparation of a INTSIG, an antibody against a INTSIG, methods of detection of INTSIG proteins or nucleic acids; an antibody against a INTSIG; containing INTSIG nucleic acids, methods of screening compounds for their acids or compositions comprising an INTSIG protein, and pharmaceutical compositions comprising them are useful in diagnosing, treating or compositions comprising them are useful in diagnosing, treating or preventing a variety of disorders, including cell profilerative disorders (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple compositions cancer or atherosclerosis); autoimmune/inflammatory disorders (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple corporations, parasitic, protozoan or helminthic infections; neurological disorders (e.g., epilepsy, stroke, Alzheimer's disease); developmental disorders (e.g., achondroplastic comparations disease); developmental disorders (e.g., achondroplastic comparations); neurological disorders (e.g., achondroplastic comparations); neurological disorders (e.g., achondroplastic comparations); neurological disorders (e.g., achondroplastic comparations); reproductive disorders (e.g., achondroplastic comparations); reproductive disorders or the hypothalamus or pituitary gland or comparations or planes or parkinson's disease, dementia, or the present sequence comparation of the hypothalamus or pituitary gland or comparation of the invention or help present sequence comparations of the present sequence comparation of the invention or the present sequence contains the present sequence contains the present sequence contains the present sequence contains an invention of the present sequence contains an invention of the present sequence co
diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents an INTSIG protein of the invention.
                                                                                                                                             Claim 1; Page 225-226; 367pp; English.
                                                                          infections.
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## Seguence 414 AA;

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                                                                                                                                                                                                                                                                                           260 CAEISSASFNW----DCSLILTGSMDKTCKLWDATNGKCVATLTGHDDEILDSCFDY 312
                                                                                                                                                                                                                                                                                                                           419
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                                                                                               --TLEGHRNVVYAIAFNNPYGDKIATG
                                                                                                                                188 SGDSŢARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDG
                                                                                                                                                              154 SFDKTCKLWSVETGK-----CYHTFR-----GHTAEIVCLSFNPOSTLVATGSMDT
                                                                                                                                                                                                                                                                                                                                                  313 TGKLIATASADGTARIFSAATRKCIAKLEGHEGEISKISF------NPQGNHLLTGSS
                                                                                                                                                                                           248 FARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTIIWDAHTGEAKQQFPFH
                                                                                                                                                                                                                          200 TAKLWDIONGEELTLRGHSAEIISLSFNTSGDRIITGSFDHTVVVWDADTGRKVNILIGH
                                                                                                                                                                                                                                                            SA--PALDVDWQSNNTFASCS---IDMCIHVCKL---GQDRPIKTFQGHINEVNAIKWDP
                                                               129 NTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAW-NPVSDLLASG
                                                                                                                                                                                                                                                                                                                           TGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASAS
                                   Gaps
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   Length 414;
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                                Indels
,DB 6;
13.8%; Score 374.5; DB 6; 28.3%; Pred. No. 5.7e-26; iive 49; Mismatches 137;
                                Conservative
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 Query Match
Best Local Similarity
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ABB62260 standard; protein; 411 26-MAR-2002 ABB62260, RESULT 12 ABB62260 ID ABB6 XX AC ABB6 XX DT 26-M XX XX

Drosophila melanogaster polypeptide SEQ ID NO 13572

SAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSD 182 LMVSASEDATIRIWDFETGEYERSLKGHTDSV-----QDVA-----FDAQGK 163 TGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIK 356 PNAN---LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKC 465 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences |:: |:||:||:|| |::|
VHIEGSIFATCSNDQTIRVWLTNSKDCKVELRDHEHTVECIAWAPEAAASAINEAAGADN **BELNQAIADYLGSNGYADSLETFRKEADLSTEVEKKFGGLLEKKWTSVIRLQKKVMELEA** 63 EVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQQAAAAAAAAAAASQQG LLASGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGT LLATGSYDGFARIW--TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAH 357 WDPTGNILASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP------TGPGTNN DEVNFLVYRYLQESGFSHSAFTFGIKSHIS---QSNINGALVPPAALISIIQKGLQYVEA -----YC----VKTYTGHREWVRMVR Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. Indels 163; Disclosure; SEQ ID NO 13572; 21pp + Sequence Listing; English Length 411; -----KEVIE------13.6%; Score 370.5; DB 4; 22.4%; Pred. No. 1.3e-25; iive 77; Mismatches 158; EE. Myers PWD, 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. ::: | KLTEAE------23-MAR-2001; 2001WO-US009231 TG----ij Conservative Drosophila melanogaster. Adams M, 2001-656860/75 Query Match Best Local Similarity Matches 115; Conserv (PEKE ) PE CORP NY WPI; 2001-656860 N-PSDB; ABL06363 Sequence 411 AA; WO200171042-A2 interactions. 27-SEP-2001 Venter JC, ø 123 122 297 183 164 g g g . g ò à g à d à ð

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RESULT 14
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303 KKGHQGPFLASGSRDKTIRIMDVSVGLCLLTLSGHDNWVRGLAFHPGGKYLVSASDDKT 362
                                                                                                                                                                                                                                                                                                              TZap; T cell activation; immune response; transplant rejection; bone marrow transplantation; rheumatoid arthritis; lupus erythematosis; buntiple sclerosis; encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis; thyroiditis; malignant disorder; asthma; lepramatosis; gastritis; skin tumour; adrenal tumour; lung tumour; wound healing; growth disorder; inflammatory disease; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polymucleotide encoding TZap protein involved in T cell activation, useful for diagnosing and treating diseases involving T cell activation, for treating organ transplantation rejection, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "unspecified residue encoded by NTC'
                                                                                                                                                                                                                                                                               of a human TZap gene cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.5%; Score 367.5; DB 4; Best Local Similarity 26.8%; Pred. No. 3.4e-25; Matches 103; Conservative 47; Mismatches 145;
                                                                                         -----DLRNKRCMKTLYAH 380
                                                    466 VHIWNTQVCLHYLNGQVLLNLGRSICLYTLPHH
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inflammatory and/or infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 56-57; 68pp; English
                                                                                                                                                                            AAB68284 standard; protein; 485
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                                                                                                                                                                                                                                                (first entry)
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N-PSDB; AAF85075.
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AAB68284
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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human guanosine triphosphate (GTP) -binding associated proteins (GBAPs; AAB68501-AAB68566) and their coding sequences (AAF58301-AAF58366). The proteins and coding sequences of the
                                                                                                                      307
                                                                                                                                                                                                                                            385
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asthma.
                        110 LEGHSEAVISVAFSPTGKYLASGSGDTTVRFWDLSTBTPHFTCKGHRHWVLSISWSPDGK
                                                                             -----QSNNTFASCS
                                                                                                                                                                                                                                                                                                                          165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                      IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH--
                                                                                                                                                   230 INDTTACRCERILIGHTQSVTCLRWGGDG-LLYSASQDRTIKVWRAHDGVLCRTLQGHGH
                                                                                                                                                                                                             289 WVNTMALSTDYALRTGAFEPAEASVNPQDLQGSLQELKERALSRYNLVRGQGPERLVSGS
                                                                                                                                                                                                                                              327 IDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH
                                                                                                                                                                                                                                                                                                        DIQOHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV
                                                            -----NKDVTSLDW-----NSEGTLLATGSYDGFAR
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Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New guanosine triphosphate-binding associated proteins (GBAP) encoding nucleic acids, useful for treating and/or diagnosing associated with GBAP expression, such as cancer, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillman JL, Lal P,
Lu DAM, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GTP-binding associated protein #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 133-134; 233pp; English
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99US-0150460P.
99US-0159849P.
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Baughn MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                  --SAPALDVDW----
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N-PSDB; AAF58316.
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23-AUG-1999;
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Reddy R,
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                                                                                                                                                                            LEGHSEAVISVAFSPIGKYLASGSGDITVRFWDLSTETPHFICKGHRHWVLSISWSPDGK
                                                                                                                                                                                                     DVPS----NSEGTLLATGSYDGFAR
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                                                                                                                                                                                                                                                                                                                                                         327 IDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH
                                                                                                                                                                                                                                                                                                                                                                                                           386 DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV
                                                                                                                                                                                                                                                                                                                                                                                                                           165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy
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present invention are useful for treating a variety of disorders including inflammation, AIDS, Addison's disease, anaemia, arteriosclerosis asthma, autoriosclerosis, asthma, autoriosclerosis, cancer, diabetes, osteoporosis and hepatitis, multiple sclerosis, cancer, diabetes, osteoporosis and
                                                                                                                             : 68
                                                                                                    Length 485;
                                                                                                                           47; Mismatches 145; Indels
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Wakamatsu A, Nagai K, Otsuki
                                                                                                    DB 4;
                                                                                                    Score 366.5; DB 4
Pred. No. 4.2e-25;
                                                                                                                                                                                                                                                                                                       --SAPALDVDW-------
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26.8%;
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11-JAN-2000; 2000JP-00118776.
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                                                                            Sequence 485 AA;
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The present invention describes primer sets for synthesising 5602 full-
length CDMAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the onligounclectide comprises at least 15 nucleotides; or. (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence of proportions and the comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence; where the repay and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDMAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDMAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDMAs. The primers allow obtaining of the full-length cDMAs easily without any specialised methods. AAH1362s and AAH13613 represent human amino acid sequences, and AAH1362 to AAH1362s represent human amino acid sequences, and AAH1362 to AAH13612 represent complements and used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LEGHSEAVISVARSPIGKYLASGSGDITVRFWDLSTEIPHFICKGHRHWVLSISWSPDGK
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                                                                                                                                              ID NO 11400; 2537pp + Sequence Listing; English.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

August 9, 2004, 16:41:43; Search time 13.3333 Seconds (without alignments) 3708.183 Million cell updates/sec

Title: Perfect score:

US-09-987-701-4 2718 1 MSISSDEVNFLVYRYLQBSG......LPHHLVVIPLVALIBLLVLK 514

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

piri: piri: pir3:\* pir4:\* PIR\_78:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		. %			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
7	475	17.5		•	AC2239	WD-40 repeat prote
2	472	•			S48268	e membrane
٣	458.5	٠			AI2155	ப
4,	451.5	•			AF2071	O)
5	444.5	•			AE1810	repeat prot
9	429.5	•			A12493	peat protein
7	426	15.7	1708	~	AE1866	repeat
ω	420.5				T18521	ransducin-l
σ	408	'n.			AD1842	O repeat prot
10	404.5	4.			AG1889	repeat prot
11	395	4.			AC1842	repeat prot
12	394.5				S76086	transducin-l
13	382.5	14.1			T40883	
14	381	14.0			AB2410	WD-repeat protein
15	698	•			AH2195	hypothetical prote
. 91	368.5				AG1837	WD-40 repeat prote
17	366				T41148	p repea
18	365	13.4			AH2154	t prot
19	354	•			AF1890	speat prot
20	349.5	12.9			S48052	platelet-activatin
21	4				AB2202	hypothetical prote
22	342				836113	LIS-1 protein - hu
23	~	12.6			AE1861	e/threonine
24	8				37	WD-40 repeat-prote
25	337				8	etical prot
26	332	12.2			덩	prot
27	m				805357	Н
28	326.5	12.0			T00798	
53	324	11.9	342	7	AE2490	t pro

WD-repeat protein	probable WD-repeat	PF20 protein, micr	hypothetical prote	probable sulfur me	WD-40 repeat prote	hypothetical prote	transcription init	TATA box-binding p	WD-40 repeat regul	hypothetical prote	hypothetical prote	MET30 protein - ye	beta transducin-li	hypothetical prote	hypothetical wp-re
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010	333 2	606 2	579 2	605 2	357 2	376 2	704 2	798 2	317 2	701 2	501 2	640 2	1049 2	370 2	777 2
589 2	11.8 333 2	11.8 606 2	11.7 579 2	11.4 605 2	11.4 357 2	11.4 376 2	11.3 704 2	11.3 798 2	11.2 317 2	11.2 701 2	11.0 501 2	11.0 640 2	11.0 1049 2	370 2	10.9 777 2

## ALIGNMENTS

		Nostoc
		1
		[imported]
		protein
1 1	•	repeat
SULT	2239	-40

RESULT 1
AC239
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
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64; Gaps Length 1526; Query Match 17.5%; Score 475; DB 2; Length 152 Best Local Similarity 31.0%; Pred. No. 7.1e-26; Matches 119; Conservative 63; Mismatches 138; Indels

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1127 NGV-TLANGSSDQIVRLWD--ISSKKCLYTLQGHTNWVNAVAFSPDGATLASGSGDQIVR 1183 195 IWNLSENS----TSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFAR 250 136 NGAHTIANNHIDMMEVDGDVEIPPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTAR à à

251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309 g  $\delta$ 셤

1285 -----NWVNSVAENPDGSMLASGSGDQTVRLWEISSSKCLHTFQGHTSWVSSVTFSPDGT 1339 362 310 PALDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGN g S

1340 MLASGSDDQTVRLWSISSGECLYTFLGHTNWVGSVIFSPDG-----AILASGSGDQ 1390 422 363 LLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDS ò g

1437 TVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQV 1391 423 ò g

--NISSGECLYTLHGHINSVRSVA 1459 483 LLNLGRSICLYTLPHHLVVIPLVA 506 1438 δ

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1683 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 PGPKGAIFVYQITEKTPTGKLIGHHGPISVLEFNDTNKLLSASDDGTLRIWHGGNGNSQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISIIQKGLQYVEAEVSINEDG----TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 qaaaaaaaaasqqqsakngentangeengahtiannhtdmmevdgdveippnkavvlr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                      probable membrane protein YBR103w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0832
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: $48268; $45971; $44683
F;Mannhaupt, G; Stucka, R; Ehnle, S;; Vetter, I; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
                                                                                                                                                                                                                     Title: Analysis of 70 kb region on the right arm of yeast chromosome II. Reference number: S48255; MUID:95208357; PMID:7900426; Accession: S48268; Accession: S48268; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 NSFYGHSQSİVSASWV------GDDKVISCSMDGSVRİMSLKQNTLLALSIVDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 VNLVQRGILYTESELMVDSKGDISALNEHHLSEDFNLVQALQID------KEKFPBI
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Reaidues: 1-535 <MAN>
A; Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55606.1; PID:g476059
R; Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A; Reference number: S45927
A; Accession: S45971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSITSBELNYLIWRYCQEMGHEVSALALQDETRVLBFDEKYKEHI------PLGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |||: : :|| | :| ||: : :|| | - KLDNIVSSTWNDLDESILAYGEKNSVARLARIVETDQBGKKYWKLTIIAELRHPFALSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGKTINQVICLAMSHDGNSIVIGVENGELREMNKIGALLNVINFHRAPIVSVKMNKDGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: unassigned WD repeat proteins; WD repeat homology C;Keywords: transmembrane protein F;355-388/Domain: WD repeat homology <WD1>F;357-429/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.4%; Score 472; DB 2; Length 53
Best Local Similarity 25.8%; Pred. No. 2.8e-26;
Matches 140; Conservative 91; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F,434-450/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Reatiues: 1-535 <FE2>
A;Cross-references: EMBL:Z35972; MIPS:YBR103w
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSISSDEVNFLVYRYLQESGFSHSA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SGD:SIF2
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AF2071
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2071
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Karneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nak Res. 9, 205-213, 2001.
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                         WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AI2155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1258 «KUR»
A;Crossreferences: GB:BA000019; PIDN:BAB74499.1; PID:g17131893; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 -----LRGHSNRVYSAIFSPNGEIIATGSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
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445 IFAGRISQDGQKYAVAFWDGQVNVYD----LKKLNSKSRSLYGNRDGILNPLP----IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 QDRPIKTFQGHTWEVNAIKWDPTGNLLASCSDDWTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            974 LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.9%; Score 458.5; DB 2; 32.0%; Pred. No. 8.5e-25; iive 43; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1204 ASGSQDQTVRIWNVKTGECLQILRAKRL 1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1074 GQLLASASADOSVRLWD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                        496 LYA 498
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                                                                               504 LVA
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d  $\delta$ q δ g à g ò g ò d à g ò Db

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WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 G;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #sequence_revision 14-Dec-2001 #sequence_revision 14-Dec-2002 C;Accession: A12493 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasada, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Reference number: AB1807; WUID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                        A;Accession: AI2493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1189 «KUR»
A;Cross-references: GB:BA000020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180
A;Experimental source: strain, PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSP 452
                                                                                                                                                                                                                                                     272 LKWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQ-SNNTFASCSTDMC 330
                                                                                                                                                REGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW----TKDGNLASTLGQHKGPIFA 271
  334 CGEDRSIKLWDIQRGECVNTLWGHSSQVWAIA-----FSPDGRTLISCSDDQTARLWDV 887
                                                                                                                                                                                  | | | | :: | : | : | | | | :: | : | 338 R-GHQG-----RIRSVAFHPDGKILASGSADNTIKLMDISDTNHSKYIRTLTGHTNMVWT
                                                                                                                                                                                                                                                                                                                                                                                  891 HKSNVNTHPFRILQGHSNRVFSVVFSSTGQLLASGSADRTIKLWSPHTGQCLHTLHGHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 NKDVTSLDWNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AGVDKTTIIWDAHTGEAKQQFPFHSAPALDV--DWQSNNTFASCSTDMCIHVCKLG----
                                                  EIPPNKAVVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCI
                                                                                                                                                                                                                                                                                                                                                        IHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTK-HQEPVYSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 LOGHOHWVKTIAFNSGGRILASGSFDQNVKLWDIH----TGKCVMTL----OGHTGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1189;
                                                                                -ITGNSLNILRGYTRDVYSVAFSPDSQILASGRDDYTIGLWNLKTGEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%; Score 429.5; DB 2; Length 1
30.3%; Pred. No. 9.7e-23;
.ive 63; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSPDGRLLASGSEDEKIQLWDMQNC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSPDGRYLASGSFDKCVHIWNTQVC 474
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Best Local Similarity
Matches 113; Conserva
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                                                                                                                                                     216
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                                                                                                        888
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
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A;Status: preliminary
A;Modecule type: DNA
A;Modecule type: DNA
A;Residues: 1-1227 <KURA
A;Cross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a1r0029
A,Cross-references: GB:BA000019; PIDN:BAB73823.1; PID:g17131215; GSPDB:GN00179 A,Experimental source: strain PCC 7120 C;Genetics: A,Genetics: A,Genetics: al12124
                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLAT 242
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                                                                                                                             16.6%; Score 451.5; DB 2; Length 1683; ilarity 28.1%; Pred. No. 4.1e-24; Conservative 75; Mismatches 167; Indels 73;
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Best Local Similarity 29.23
Matches 130; Conservative
                                                                                                                                                        Similarity
                                                                                                                                                                                Matches 123;
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A; Cross-references: EMBL: L28125; NID: 9607002; PID: 9607003; PIDN: AAA85775.1
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                                         C,Genetics:
A,Gene: het-e1
A,Introns: 761/3
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C;Species: Podospora anserina
C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18521
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Begueret, J.
R;Saupe, S.; Turcq, B.; Bolospora anser
R;Sature: preeliminary; translated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Residues: 1-1356 <SAU>
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1866
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A Modecule type: DA
A Modecule type: DA
A Residues: 1-1708 «KUR»
A; Cross-references: GB:BA000019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Gen
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15.7%; Score 426; DB 2; Length 17
Best Local Similarity 32.1%; Pred. No. 2.9e-22;
Matches 110; Conservative 61; Mismatches 130; Indels
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DGRYLASGSFDKCVHIWN--TQVCL
                                                                                                                                                                                                                                                                                                     :|: :|: |
1062 IGKGVCVRTFSGH 1074
                                                                                                                                                                                                                             LGRSICLYTLPHH
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453
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1010 GSVWSVAFSPDGQRVASGSDDKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                     12;
                                                                                                                                                                                      820 ISTISVVEABWNACTQT-----LEGHGSSVLSVAFSADGQRVASGSDDKTIKIWDT 870
                                                                                                                                                                                                                                                                             ANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD 190
                                                                                                                                                                                                                                                                                                                                                                                                                 191 STARIMNLSENSTSGS-TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 KTIKIW----DAASGTCTQTLEGH----GGR-----VQSVAFSPDGQRVASGSDDHTI 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 SDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW 427
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A;Residues: 1-1711 (KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77808.1; PID:g17135262; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AHTIANNHIDMMEVDGDVEIPP 159
                                                                                                                                                                                                                                                                                                                      APALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GOTIVSA
                                                                                                                                          78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAASQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEG 1175
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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN--TQVCLHYLNG 480
       Length 1356;
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                                                                     Indels
15.5%; Score 420.5; DB 2;
llarity 28.2%; Pred. No. 5.2e-22;
Conservative 63; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
15.0%; Score 40%; DB 2; L.
Best Local Similarity 26.2%; Pred. No. 5.7e-21;
Matches 125; Conservative 76; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::|||:
| SASDDGTIRLWSLDGRPLITIPSHTKQVLAVTFSPD-
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Db 533 NGVNSVTESPDGKLIATASGDRTVKLWNSKGQE-LETLYGHTDAVNSVAFSPDGTSIATA 591  Oy 406TUNPNANLMM	A; Reference mumber: AB1807; MUID:21595285; PMID:11759840 A; Accession: AC1842 A; Accession: AC1842 A; Accession: AC1842 A; Molecule type: DNA A; Residues: 1-1747 < KCR> A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179 A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179 A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179 A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179 A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Best Local Similarity 28.2%; Pred. No. 5.1e-20; Matches 105; Conservative 59; Mismatches 131; Indels 78; Gaps 9 A; Genetics: Best Local Similarity 28.2%; Pred. No. 5.1e-20; Attention of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the conservative Formation of the co	Db 1370 LVSAGADSTMKVMKIDGTLIKTISGRGEQIRDVTFSPDNKVIASASSDKTVRIRQLNYGK 1429  Cy 227DVTSLDWNSEGTLLATGSYDGPARIWTKDGNLASTLGGHKGPIFALKKNKKG 278  Db 1430 GQKSNVNSEVBPGKTPASAGWDGNITIWQRE-TLAHSSLSTICKNGNITITYSYSPG 1488  Cy 279 NPILASGCWRTTIIWDAHTGEAKQPFPRAPALDVWQ-SNNTFASGTDMCHVCKLG 337  Db 1489 KTIATASADNTIKLWDSGTQGLIKTTTGFHPDNGTLASGSADKTIKIWRVN 1548  Cy 338 QDRPIKTFGGHTNEVNAIKWDPTGNLASGSDMTLKIWSMKQDNCVHDLQQHNKEIYTI 397  Db 1549 DGGLLRTLGHNBVNSTSPDGGPLASGSDMTLKIW-OTDGRLIKNITGHCLAISV 1607  Cy 398 KWSPTGPGTNNPNAMLMLASASPDGTPLASGSDMTLKHWQPTDGRLIKNITGHCLAISV 1607  Cy 398 KWSPTGPGTNNPNAMLMLASASPDGTVRLWDVDGKLINNLNGHIDGVTGLSFSPDGBIL 1658  Cy 458 ASGSPDKCVHINN 470  Db 1659 ASGSDNTIKLWN 1671  RESULT 12  ST6086  Deta transducin-like protein, 190K - Synechocystis sp. (Strain PCC 6803)  N;Alternate names: protein sl10163  C;Specias: Synechocystis sp.  A;Variety: PCC 6803  C;Date: 25-Apr-1997 #text_change 26-May-2000  C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
	RESULT 10 AG1889 WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. PCC 7120 C;Date: Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001 A;Tele: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium AA;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Status: preliminary A;Residues: 1-934 *KURA A;Residues: 1-934 *KURA A;Residues: 1-934 *KURA A;Residues: 1-934 *KURA A;Residues: 1-934 *KURA A;Residues: 1-934 *KURA A;Genetics: A;Genetics: A;Genetics: A;Genetics:	Query Match Best Local Similarity 24.1%; Score 404.5; DB 2; Length 934; Best Local Similarity 24.1%; Pred. No. 4.4e-21; Matches 124; Conservative 104; Mismatches 176; Indels 111; Gaps 19;  8

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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 RDKLAQQQAAAAAAAAASQQGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI
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14.5%; Score 394.5; DB 2;
Best Local.Similarity 28.2%; Pred. No. 5.3e-20;
Matches 115; Conservative 55; Mismatches 149;
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WD repeat homology (WD04)
WD repeat homology (WD05)
WD repeat homology (WD05)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1584-1617/Domain: WD
F;1625-1658/Domain: WD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F)1256-1289/Domain: W
F)1297-1330/Domain: W
F)1338-1371/Domain: W
F)1420-1453/Domain: W
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F;1174-1207/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1461-1494/Domain:
E;1502-1535/Domain:
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WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)

WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)

WD-repeat protein [imported] - Nostoc sp. PCC 7120

A,Note: Nostoc sp. Strain PCC 7120

A,Note: Nostoc sp. Strain PCC 7120

A,Note: Nostoc sp. Strain PCC 7120

S,Coession: AB2410

B,Xanako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S.

BNA Res. 9, 205-213, 2001

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anath A,Reference number: AB1807; WUID:21595285; PMID:11759440

A,Reference number: AB1807

A,Molecule type: DNA

A,Molecule type: DNA

A,Residence: 1-1551 (KUR>

A,Residence: 1-1551 (KUR>

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A,Residence: 1-1551 (KUR>

A,Residence: 1-1551 (KUR>

A,Residence: Strain PCC 7120
A;Cross-references: EMBL:AL031764; PIDN:CAA21113.1; GSPDB:GN00066; SPDB:SPCC1235.09
A;Experimental source: strain 972h-; cosmid c1235
C;Genetics:
A;Gene: SPDB:SPCC1235.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPTGNILASCSDDMTLKIWSMKQD---NCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLM 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VELEKHYVDNHSSNEEASKTSIDGE----SLVNENPCKLPFYLTVPHICETTLTKADST 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ICA-WNPVSD----LLA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAK 301
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14.0%; Score 381; DB 2; Length 1551;
Best Local Similarity 23.4%; Pred. No. 4.4e-19;
Matches 118; Conservative 94; Mismatches 175; Indels 118;
                                                                                                                                                                                                                                                                             Indels 101;
                                                                                                                                                                                                                    564;
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                           Query Match
Best Local Similarity 24.4%; Pred. No. 8.5e-20;
Matches 131; Conservative 106; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 NNHIDMMEVDGDVEIPPNKAVVLRGHE---SEVF-
                                                                                                                                                               A; Introns: 18/1; 273/3; 413/3
                                                                                                                                      A; Map position:
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A,Gene: all4834
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Qy 168 HESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKD 227  Db 390 HASIVNSVAFENGETELASGSDDKIIKVNNLKN		
99 48 ALISHOKGLOYVEAEVSINEDGRPIESISLIDAWPDVVOTRODAYRDKLAGOO 107 Db 903 ALWSAWRSGKALQALVKDGRSLAKYPATSPLLALGTILDNIGERNQPQGHQ 953 QY 108 AAAAAAAAAASQGGSAKWGENTARYPATSPLLALGTILDNIGERNQPQGHQ 953 QY 108 AAAAAAAAAAASQGGSAKWGENTARNOHTDNINHTDNINHTDNINTAVLRG 167 Db 168 HESEVEIANDHWYSDLAGSGSDSTARTWILSENSTSGSTGDVLRHGIR 216 H ::	RESULT 15 AH2195 Hypothetical protein alr3119 [imported] - Nostoc sp. (strain PCC 7120) C,Species: Nostoc sp. PCC 7120 C,Species: Nostoc sp. PCC 7120 C,Date: Nostoc sp. strain PCC 7120 C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C,Accession: AH2195 R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.	Ouery Match Best Local Similarity 23.7%; Pred. No. 1e-18; Best Local Similarity 23.7%; Pred. No. 1e-18; Matches 116; Conservative 96; Mismatches 194; Indels 84; Gaps 13;  Qy 21 FSHSAFTFGIKSHISGSNINGALVPPAALISIIQKGLQYVEAEVS 65

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec August Run on:

Title: Perfect score:

US-09-987-701-4 2718 1 MSISSDEVNFLVYRYLQESG......LPHHLVVIPLVALIELLVLX 514 Sequence:

**BLOSUM62** Scoring table: 141681 seqs, 52070155 residues Searched:

Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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TU12 SCHPO	SCOB_EMENI FW1A_HUMAN	YZLL CAEEL FW1B HUMAN	LUG ĀRATH TUPI KLULA	PRP4_ARATH GBB MAIZE	TU11 SCHPO PRP4 HUMAN
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586 395	678	395 542	931 682	3.84 3.80	614 522
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288.5	286	283 283	283 282.5	281 280.5	280
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### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND INTERACTION WITH HDAC3.
MEDLINE-21930350; PubMed-11931768;
Zhang J., Kalkum M., Chait B.T., Roeder R.G.;
"The N-COR-HDAC3 nuclear receptor corepressor complex inhibits the JNK pathway through the integral subunit GPS2.";
Mol. Cell 9:611-623 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

Matsumawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

Matsumawa H., Nagahari K., Masuho Y., Sasaki N.;

Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMDINIT: Interacts with HDAGC3.

-!- SIMDINIT: Interacts with HDAGC3.

-!- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang X., Dormady S., Basch R.;
"Identification of four human to by early hematopoietic progenitors.";
Submitted (MAY-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                       Q9BZK7; Q9H2I1; Q9H9A1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1 (TBL1-related protein 1).
                                          514 AA.
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF214544; AAK00301.1; --
EMBL; AF228193; AAG44736.1; --
EMBL; AK022956; BAB14331.1; --
InterPro; IPR006594; LisH.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8
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ProDom; PD000018; WD40; 3.
SMART; SM00667; LiSH; 1.
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                          TBLR HUMAN
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                                                                                                                                                                                                                                                                                                                                                                        61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAASQ
                                                                                                                                                                                                                                                                                                          1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                  Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)
TBLIX OR TBLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                            -> K (IN REF. 2).
-> H (IN REF. 3).
-> Q (IN REF. 2).
0ESSGDZEE4BA796D CRC64;
                                                                                                                                                                                                                                                         Score 2493; DB 1;
Pred. No. 2.4e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 AA.
                                                                                                                                                                                                                                                                                  1; Mismatches
          PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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SM00320; WD40; 8.
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                                                          Repeat; WD repeat.
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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                        MEDLINE=99264241; PubMed=10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.;
"X-linked late-onset sensorineural deafness caused by a deletion involving OA1 and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616(1999).
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PROSITE; PS50896; WD.REPEATS_1; 4.
PROSITE; PS50082; WD.REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL, BC032708, AAH32708.1; -...
Genew, HGNC:11585, TBLIX.
                                                                                                                                                                                         TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932;
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ProDom: PD000018; WD40; 3.
SMART; SM0067; LisH; 1.
SMART; SM00320; WD40; 7.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
TBLIY OR TBLI.
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Kuroda-Xawaguchi T., Skaletsky H., Minx P.J., Brown L.G., Rozen Wilson R.K., Waterston R.H., Page D.C.;

"The DNA sequence of the human Y chromosome.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 LisH domain.
-! SIMILARITY: Contains 8 WD repeats.
                                                    14;
       Length 526;
                                                 Indels
Query Match
82.0%; Score 2229; DB 1;
Best Local Similarity 85.4%; Pred. No. 4.4e-155;
Matches 414; Conservative 32; Mismatches 25;
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61 BAEISINKDGTVFDSRPIESLSLIVAVIPDVVQMRQQAFGEKLTQQQASAAATEASAMAK 120
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Pred. No. 8.7e-151;
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(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches
                                                                                                                                  PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD REPEATS_1; 4.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                      LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 6.
                                              Pfam; PF00400; WD40; 8.
PRINTS; PR00320; GPROTEINBRPT.
PRODOM; PD000018; WD40; 3.
SWART; SM00667; Lish; 1.
SWART; SM00320; WD40; 8.
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Genew, HGNC:18502, TBL1Y.
InterPro, IPR006594; LisH.
InterPro, IPR001680; WD40.
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DOMAIN 4
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16-OCT-2001
10-OCT-2003
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TBLX_MOUSE
ID TBLX M
AC Q9QXET
DT 16-0CT
DT 16-0CT
DT 10-0CT
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9 9

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251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
 (Rel. 41, Last annotation update)
     Hypothetical WD-repeat protein alr3466.
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BIR; ACC299; ACC239.
INCEPPC; IPR007111; NACHT_NTPASE.
INCEPPC; IPR001680; WD40.
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901
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Matches 119; Conserv
 28-FEB-2003
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                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GSYDGFARIWTKDGNLASTLGOHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 NILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEG-----TLLAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFPFHS-APALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Transducin beta-like 1X protein (Fragment).

TBLIX OR TBL1.

Was musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQV 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston Hunter G., Kimberly C., Rhodes M., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ:databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 1308; DB 1; Length 313; 83.2%; Pred. No. 3.2e-88; ive 16; Mismatches 19; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34808 MW; 3BC48683432DFEF7 CRC64;
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(Rel. 41; Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO0320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
SMART; SM00320; WD40; 5.
FROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50244; WD REPEATS 2; 4.
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                                                                                                                                                                MEDLINE=21595285, PubWed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Irigurin M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakada W., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Sanda M., Tabata S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M., Sanda M.
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PEDDOM; PRO0320; GRACHEINBRPT.

PRODOM; PRO0320; WD40; 15.

SMART; SM00320; WD40; 15.

SMART; SM00320; WD40; 15.

PROSTIE; PS00678; WD REPERATS 1; 11.

PROSITE; PS500294; WD REPERATS 2: 15.

PROSITE; PS500394; WD REPERATS REGION; 1.

Hypothetical protein; Repeat; WD repeat; Complete protecome. REPEAT
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1069 WD 6.

1111 WD 7.

1153 WD 9.

1279 WD 11.

1321 WD 12.

1321 WD 12.

1405 WD 14.

1447 WD 15.

1491 WD 15.

1491 WD 16.
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
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31.0%; Pred. No. 1.5e-26;
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50 ISIIQKGLQYVEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG 219
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                                                                                                                                                                   R GO; GO: 0005634; C:nucleus; IPI.
R GO; GO: 0005634; C:nucleus; IPI.
R GO; GO: 0017136; F:NAD-independent histone deacetylase activity; IDA.
R GO; GO: 0017136; F:NAD-independent histone deacetylase activity; IDA.
R GO; GO: 001575; F:NAD-independent histone deacetylase activity; IDA.
R GO; GO: 0016575; P:nictome deacetylation; IDA.
R GO; GO: 0016575; P:nictome deacetylation; IDA.
R GO; GO: 0016575; P:nictome deacetylation of transcription from P. . .; IPI.
R GO; GO: 0016575; P:negative regulation of transcription from P. . .; IPI.
R InterPro; IPRO01680; W440.
R InterPro; IPRO0108; W440.
R Prodom; PD000018; W440.
R SMART; SM00367; Lish; 1.
R SMART; SM0320; W440; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 VNLVQRGILYTESELMVDSKGDISALNEHLSEDFNLVQALQID-----KEKFPEI
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25DD19AB2BFB4B07 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSSO896; LISH; 1.
PSSO867; LISH; 1.
PSSO0678; WD_REPEATS_1; FALSE_NEG.
PSSO082; WD_REPEATS_2; 4.
PSSO294; WD_REPEATS_REGION; 1.
WD_repeat; Chromatin_regulator; Nuclear protein.
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                                              : :
                                      EMBL, X78993, CAA55606.1,
EMBL, Z35972, CAA85058.1,
PIR, S48268, S48268.
GermOnline; 138646; -.
SGD, S0000307; SIF2.
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1340 MLASGSDDQTVRLWSISSGBCLYTFLGHTNWVGSVIFSPDG-----AILASGSGDQ 1390
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                                                                                                                                                                                                                                                                                                       TVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQV 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95208357; PubMed=7900426;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1281 (1994).
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                                                                                                                                                                                           363 LLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDS
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Pijnappel W.W.M.P., Schaft D., Roguev A., Shevchenko A., Tekotte H., Wilm M., Rigaut G., Seraphin B., Asaland R., Stewart A.F.;
Hors S. Cerevisiae SET3 complex includes two histone deacetylases,
Hos2 and Hstl, and is a meiotic-specific repressor of the sporulation gene program.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cockell M., Renauld H., Watt P., Gasser S.M.;
Siffo interacts with Sir4p amino-terminal domain and antagonizes
telomeric silencing in yeast.";
Curr. Biol. 8:787-790(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION IN A COMPLEX WITH HOS2; HST1; SNT1; CPR1; YIL112W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                            TVRLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLW----
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01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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SIF2 OR EMBI OR YBR103W OR YBR0832.
                                                                                                                                                                                                                                                                                                                                                                                                                LLNLGRSICLYTLPHHLVVIPLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98315485; PubMed=9651685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIF2 YEAST
ID SIF2 YEAR
AC P38262;
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101

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                  495
445 IFAGRISQDGGKYAVAFMDGGUNVYD----LKKLNSKSRBLYGNRDGILNPLP----IP
                                                                                                                                                                                                                                                                                                                    MEDLINE=21955285; PubMed=11759840; Karitz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikava A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; Complete SI-205-213(2001).

SIMILARITY: Contains 1 NB-ARC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGN. PEROLOGO, MUAGO.

PÉGN. PRO0931, NB-ARC; 1.

PÉGN. PRO0403, MD40; 1.

PRINTS; PR00320; WD40; 1.

PRODOM; PD000018; WD40; 1.

PROSITE; PS00320; WD40; 1.

PROSITE; PS0032; WD REPEATS 1; 9.

PROSITE; PS00294; WD REPEATS 2; 14.

PROSITE; PS0294; WD REPEATS RECION; 1.

HYPOTHATICAL PROCEST.

PROSITE; PS0294; WD REPEATS RECION; 1.

PROSITE; PS0294; WD REPEATS RECION; 1.

PROSITE; PS0294; WD REPEATS RECION; 1.
                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45DF03B91170C451 CRC64;
                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical WD-repeat protein alr2800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWD 2.2. WWD 5.3. WWD 5.4. WWD 9.7. WWD 9.1. WWD 112. WWD 112. WWD 112. WWD 114. WWD 114. WWD 115. WWD 115. WWD 115.
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InterPro; IPR002182; NB-ARC.
InterPro; IPR001680; WD40.
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                                                                       496 LYA 498
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Length 1258;

DB 1;

Score 458.5;

16.98;

Query Match

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1020 -----TDWVXAVVFHPQGKIIATGSADCTVKLMNISTGQCLKTLSEHSDKILGMAWSPD 1073
                                                                                                                                                                                                                                                                             1074 GQLLASASADQSVRLWD----- 1099
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                                                                     165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS 224
                                                                                                                                                     225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGOHKGPIFALKWNKK 277
                                                                                                                                                                                                                                     278 GNFILSAGVDKTTIIWDAHIGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                                                                                                                                                                                                        398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYL 457
                                                                                                                                                                                                                                                                                                                        338 ODRPIKTFOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKODNCVHDLOOHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                             1100 -----LRGHSNRVYSAIFSPNGEIIATCŚTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Romplete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
-!- SIMILARITY: Contains 13 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; Intervace.

Pfam. PF00400; WD40; 14.

PRINTS; PR00320; WD40; 14.

SWART; SW00320; WD40; 14.

PROSITE; PS0082; WD_REPEATS 1; 3.

PROSITE; PS50082; WD_REPEATS 2; 14.

PROSITE; PS50294; WD_REPEATS 2; 14.

PROSITE; PS50294; WD_REPEATS REGION; 1.

PROSITE; PS50294; WD_REPEATS REGION; 1.

PROSITE; PS50294; WD_REPEATS REGION; 1.

PROSITE; PS50294; WD_REPEATS REGION; 1.

REPEAT 1070 1109 WD 1:
        32.0%; Pred. No. 1.9e-25;
tive 43; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1683 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1204 ASGSODOTVRIWNVKTGECLOILRAKRL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 ASGSFDKCVHIWN -- TQVCLHYLNGQVL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21595285; PubMed=11759840;
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PIR; AF2071; AF2071.
InterPrc; IPR001680; WD40.
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=103690;
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SIMILARITY: Contains 10 WD repeats. SIMILARITY: Contains 1 NACHT domain.
                                                                                                                       PIR; T18521; T18521.
InterPro; IPR007111; NACHT NTPase.
InterPro; IPR001680; WD40.
                                                                                                               EMBL; L28125; AAA85775.1; -.
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| ASG--TGTQT------
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1091 11
1133 11
1175 12
1217 12
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117; Conserv
                     -!- SIMILARITY:
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SEQUENCE
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Best Local
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                                                                                                                                                                          LSFSPDGKTLASASADKTIKLWRIADGKLVKT-LKGHNDSVWDVNFSSDGKALASASRDN 1303
                                                                                                                                                                                                                ----TFTGHSGGVYAVNFLPDSN 1335
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                                                                                                                                                        64 VSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAASQQG 122
                                                                                                                                                                                            SAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSD 182
                                                                                                                                                                                                                                LLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLAT 242
                                                                                                                                                                                                                                                                     243 GSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAK 301
                                                                                                                                                                                                                                                                                                         302 QOFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                                                                                                                                                                                                                                                                             GNILLASCSDDWTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF 420
                                                                                                                                                                                                                                                                                                                                                                                            Saupe S., Turog B., Begueret J.;
"A gene responsible for vegetative incompatibility in the fungus
Podospora anserina encodes a protein with a GTP-binding motif and G
beta homologous domain.";
Gene 162.135-139 (1995).
-!- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
SPECIFIC INTERACTIONS WITH DIFFERENT ALLBLES OF THE UNLINKED GENE,
                                                                                                                                                                                                                                                                                                                                                                                 DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNG
                                                                                                                                          Gaps
                                                                                                                                        73;
                                                                                                                       Length 1683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
NCBI_TaxID=5145,
                                                                                                                                        Indels
                                                                                                    185459 MW; F7CB361FF54F7137 CRC64;
                                                                                                                      DB 1;
                                                                                                                                      75; Mismatches 167;
                                                                                                                    Score 451.5; DB
Pred. No. 9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
incompatibility protein HET-E-1.
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1336 IIASASLDNTIRLWQRPLISPL-----
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MEDLINE=96009891; PubMed=7557402;
1604 HLLT------TLPQH 1612
                                                                                                                                                                                                                                                                                                                                                                                                                     481 QVLLNLGRSICLYTLPHH 498
                                                                                                                   16.6%;
28.1%;
                                                                                                                              al Similarity 28.1
123; Conservative
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                           1359
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1609
1650
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                                                      1444
1486
1528
1570
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15-JUL-1998
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   950 KIWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHG 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820 ISTISVVEAEWNACTOT-----LEGHGSSVLSVAFSADGORVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAQQGSAKNGE-----NŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 WD 2.
953 WD 3.
955 WD 5.
1037 WD 6.
1121 WD 6.
1120 WD 9.
1163 WD 9.
1247 WD 10.
1247 WD 10.
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28.2%; Pred. No. 1.2e-22;
Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                 PÉAM; PF05729; NACHT; 1.
PÉAM; PF05729; NACHT; 1.
PÉAM; PF00400; WD40; 10.
PRINTS; PF00320; GPROTEINBRPT.
PCDOM; PD000018; WA40; 10.
PROSITE; PS06032; WD40; 10.
PROSITE; PS06037; NACHT; 1.
PROSITE; PS00038; WD_REPEATS_2; 10.
PROSITE; PS00038; WD_REPEATS_2; 10.
PROSITE; PS50034; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROSITE; PS50024; WD_REPEATS_2; 10.
PROMAIN 294 629 NACHT.
REPEAT 839 861 911 WD 2.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 RDKLAQQQAAAAAAAAAAQQGGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 PPNKAVVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIRE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                        MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
Surekovaria A., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.,
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2.153-166(1995).
-!- SIMILARITY: Contains 16 Wb repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 394.5; DB 1; Length 1693;
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PROBLE: P800020; WD40 F16.
PROSITE: P800082; WD_REPEATS 1; 8.
PROSITE; P850082; WD_REPEATS 2; 15.
PROSITE; P850294; WD_REPEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1053 1083 WD 1.
1054 1042 WD 1.
1055 1083 WD 2.
1135 1165 WD 5.
117 1247 WD 6.
1259 1329 WD 7.
1340 1370 WD 9.
1341 1411 WD 10.
1463 1493 WD 12.
1545 1575 WD 13.
1545 1575 WD 13.
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                                                                                                           Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e-20;
                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein $110163.
                      PRT; 1693 AA.
                                                                                                  Symechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008941; TPR-like.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 16.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 13.
                                                                                                                                                                                                                                                                                                                                         EMBL; D63999; BAA10064.1; -.
PIR; S76086; S76086.
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                       STANDARD;
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Matches 115; Conserv
                                                                                                                    NCBI TaxID=1148;
                       SYNYS
                                                                                                              Bacteria;
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1464 ----YEKNIFAAEFSADGQFIVTASDDNTAGIWEIVGREVGICRGHEGPVYFAQFSAD 1517
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XX MEDLINE=22388557; Pubmed=12477932;
XX MEDLINE=22388557; Pubmed=12477932;
XX MEDLINE=22388557; Pubmed=12477932;
XX MEDLINE=22388557; Pubmed=12477932;
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Marusina K., Barmer A.A., Rubin G.M., Hong L.,
XX Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Altschul M.J., Usdin T.B., Prothiyuki S., Carninci P., Prange C.,
XX Altana S.S., Loquellano N.A., Preters G.J., Abramson R.D., Mullahy S.J.,
XX Boak S.A., McGhan P.J., McKernan K.J., Malek J.A., Cunarathe P.H.,
XX Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Ilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
XX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
XX Chriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
XX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
XX Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
XX Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
XX Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
XX Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
XX Human and mouse cDNA sequences.";
XX Human and mouse cDNA sequences.";
XX Human and mouse cDNA sequences.";
XX Human and mouse cDNA sequences.";
XX Human and mouse cDNA sequences.";
218 GGQDVPSNKDVTSLDWNSEGTLLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKK 277
                                                                                                                                                                                                     278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
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Ninomiya K., Lwayanagi T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE-21064499; PubMed=11124703;
Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1645 LTSSADGTAKLWPVKTLPQLLSQGGQWLKNY-----LTHNALVSP 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 ASGSFDKCVHIWNTQVCLHYLN--GQVLLNLGRSICLYTLPHHLVVIP 503
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
WD-repeat protein HUSSY-07.
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse)
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PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 7.
SMART; SW00320; WD40; 8.
PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50294; WD REPEATS 2; 7.
PROSITE; PS52294; WD REPEATS RECION; INCLEAR protein; Repeat; WD repeat.
                                                               460 YAVDWSPDGQRVASGGKDKCLRIW 483
                                             446 YSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC018399, AAH18399.1, -.
InterPro; IPR001632, Gprotein_B.
InterPro; IPR001680; WD40.
Ffam, PP00400; WD40; 8.
                                                                                                                                             STANDARD;
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                                                                                                                                             MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 İMDITAGRCERILIGHIQSVICLRMGGDG-LLYSASQDRIIKVWRAHDGVLCRILQGHGH 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SAPALDVDW-----QSNNTFASCS 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFTLFLWSPAEDKKFLTRWIGHQALINQVLFSPDSRIVASASFDKSIKLWDGRIGKYLA 408
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                                                             WEDLINE-231727; PubMed=12429849; MEDLINE-231727; PubMed=12429849; SEDLINE-231727; PubMed=12429849; SCOURTINE-231727; PubMed=12429849; SCOURTINE-231727; PubMed=124., Courter N., Denc C., Calle A., Kindbeiter K., Sanchez J.-C., Greco A., Hochstrasser Den C., Diaz J.-J.; Fubmed=1 proteconic analysis of human nucleolus."; Mol. Biol. Cell 13:4100-4109 (2002).
-i SUBCELLULAR LOCATION: Nuclear; nucleolar.
-i SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NKDVTSLDW-----NSEGTLLATGSYDGFAR
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Cannata N., Zimbello R., Lanfranchi G., Valle G.;
"Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.5%; Score 366.5; DB 1; Length 485; 26.8%; Pred. No. 2.7e-19;
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                                                                                                                                                                                                                                                                                                   EMBL; AKO01320; BAA91621.1; ---
EMBL; BC002884; AAH02884.2; --
EMBL; BC002807; AAH10284.2; --
EMBL; AJ00527; CAA6444.1; ---
EMBL; AJ00527; CAA6444.1; ---
SWISS-2DPAGE; O9NYX2; HUWAN.
INTEPPO; IPRO01632; Gprotein_B.
INTEPPO; IPRO01680; WD40.
PRINTS; PR00319; GPROTEINB.
PRINTS; PR00319; GPROTEINB.
PRODOM; PD000018; WD40; 8.
PROSTIE; PS00088; WD REPEATS 1; 4.
PROSTIE; PS00084; WD REPEATS 2; 7.
PROSTIE; PS0092; WD REPEATS 2; 7.
PROSTIE; PS0092; WD REPEATS 2; 7.
PROSTIE; PS0092; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
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PROSTIE; PS0094; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
PROSTIE; PS0094; WD REPEATS 2; 7.
PROFEAT 112 112 MD 1.
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                          yeast sequences.";
Yeast 18:69-80(2001).
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                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIST HUMAN STANDARD; PRT; 409 AA.

P43034; Q8WZ88; Q8WZ89;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH alpha) (Lissencephaly-1 protein) (LIS-1).
PAFAHIBI OR PAFAHA OR LISI OR MDCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reiner O., Carrozzo R., Shen Y., Wehnert M., Faustinella F.,
Dobyns W.B., Caskey C.T., Ledbetter D.H.;
"Isolation of a Millar-Dieker lissencephaly gene containing G protein
beta-subunit-like repeats";
Nature 364:717-721
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=97217774; PubMed=9063735;
Lo Nigro C., Chong S.S., Smith A.C.M., Dobyns W.B., Carrozzo R.,
                                                                                                                                                                Length 485;
                                                                                2D7F59D603AEC07B CRC64;
                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                    48; Mismatches 145;
                                                                                                                                                                     13.4%; Score 365.5; DB 1
26.6%; Pred. No. 3.2e-19;
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WD 7.
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MEDLINE=93361119; PubMed=8355785;
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451 WD
484 WD
53148 MW;
                                                                                                                                                                Query Match
Best Local Similarity 26.6%
Matches 102, Conservative
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412
454
485 AA;
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SEQUENCE FROM N.A.
TISSUE=Liver;
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microtubules.
TISSUE SPECIFICITY: Fairly ubiquitous expression in both the frontal and occipital areas of the brain.
DISEASE: Defects in PAFAHIB1 are the cause of classical lissencephaly-1 (LIS1) [MIM:607432]. LIS1 is a brain malformation
                                                                                                                                                                                                                                                    MEDLINE-20512525; PubMed=11056532; Faulkner N.E., Dujardin D.L., Tai C.-Y., Vaughan K.T., O'Connell C.B., Wang Y.-L., Vallee R.B.; "A role for the lissencephaly gene LIS1 in mitosis and cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-99371784; PubMed-10441340; Pilz D.T., Kuc J., Matsumoto N., Bodurtha J., Bernadi B., Pilz D.T., Kuc J., Matsumoto N., Bodurtha J., Bernadi B., Tassinari C.A., Dobyns W.B., Ledbetter D.H.; Suboortical band heterotopia in rare affected males can be caused by missense mutations in DCX (XIIS) or LIS1."; Hum. Mol. Genet. 8:1757-1760(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21938534; PubMed=11940666; Coquelle F.M., Caspi M., Cordelieres F.P., Dompierre J.P., Coquelle F.M., Caspi M., Cordelieres F.P., Hoogenraad C.C., Akhmanova A., Dujardin D.L., Koifman C., Martin P., Hoogenraad C.C., Akhmanova A., Galjart N., De Mey J.R., Reiner O.; "LIS1, Cill-170's key to the dynein/dynactin pathway."; Mol. Cell. Biol. 22:3089-3102(2002).
                                                                                                                                                                       Wambutt R., Heubner D., Mewes H.-W., Weil B., Amid C., Osanger Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     SUBCELLULAR LOCATION, AND INTERACTION WITH DYNEIN AND DYNACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS LISI SER-30; SER-161 AND HIS-316.
MEDLINE-21394321; PubMed=11502906;
Leventer R.J., Cardoso C., Ledbetter D.H., Dobyns W.B.;
Lisi missense mutations cause milder lissencephaly phenotypes including a child with normal IQ.";
Zhao M.J., Xia S.L., Li T.P., "High expression of the lissencephaly gene in hepatocarcinoma "High expression of the lissencephaly gene in hepatocarcinoma
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21898370; PubMed=11889140;
Tai C.-Y., Dujardin D.L., Faulkner N.E., Vallee R.B.;
"Rolle of dynein, dynactin, and CLIP-170 interactions in LIS1
Kinetochore function.";
J. Cell Biol. 156:959-968(2002).
                                             Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                            Feng Z., Zhang B., Peng X., Yuan J., Qiang B.; submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELEULAR LOCATION, AND INTERACTION WITH RSN.
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                                                                                  SEQUENCE FROM N.A.
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Considered by Abhornin Tentonal Migration 2 secondary generation.

Considered by Abhornin Tentonal Migration 2 secondary decreased to the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of common state of the case tentonal lamination of the case tentonal lamination of the case tentonal lamination of the case tentonal lamination of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case tenton state of the case te
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126 NGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLA 185
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                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1).
PAFAHIBI OR PAFAHA OR LISI.
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FTId=VAR 015389.

H -> R (in L1S1).

FTId=VAR 01724.

G -> S (in L1S1).

FTIG=VAR 01739.

S -> P (in E181).

FTIG=VAR 01539.

FTIG=VAR 010203.

D -> H (in L1S1).

FTIG=VAR 010203.

D -> H (in L1S1).

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                                                                                                                                                                                                                                                                                                                                                  Nature 370:16-218 (1994)

Nature 370:16-218 (1994)

-!- FUNCTION: Probably involved in nuclear migration during cell division. Participates in the process of neuronal cell division. Participates in the process of neuronal cell division. Participates in the process of neurons. May participate in nuclear migration of differentiating neurons. May participate in targeting cytoplasmic dyrein to the microtubule plus ends, thereby playing an essential role in dynein-mediated microtubule sliding. Non-catalytic subunit of a acetylhydrolase complex, a complex that inactivates platelet-activating factor (PAF) by removing the acetyl group at the SN-2 position (By similarity).

-!- SUBUNIT: Cytoslic PAF-AH IB is formed of three subunits of 45 kDa of the enzyme resides in the beta and gamma subunits of 45 kDa of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. Interacts with dynein and dynactin. Interacts with RSN (By similarity).

-!- SUBCELULAR LOCATION: Cytoplasmic; localizes to the plus end of microtubules (By similarity).

-!- SIMILARITY: Contains 7 WD repeats.
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R InterPro; IPR001680; WD40.

R InterPro; IPR001680; WD40.

R FRIM; PR000400; WD40; 7.

R PRINTS; PR00320; GPROTEIRRPT.

R SWART; SM00320; WD40; 7.

R PROSITE; PS00649; MD REPEATS.1; 4.

R PROSITE; PS00679; MD REPEATS.2; 7.

R PROSITE; PS00679; WD REPEATS.2; 7.

R PROSITE; PS00679; WD REPEATS.2; 7.

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R PROSITE; PS00679; WD REPEATS.2; 7.

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R PROSITE; PS00679; WD REPEATS.2; 7.

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Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                               Hattori M., Adachi H., Tsujimoto M., Arai H., Inoue K.; "Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activating factor acetylhydrolase.";
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WD 2.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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410 NANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW 469
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                                                                                                            -----IPRPPEK-YALSGHRSPVTRVIFHPVFSVMV 123
                                                                                                                                                  SGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLA 241
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MEDIANE-22388257; PubMed-12477932;

MEDIANE-22388257; PubMed-12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,

Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
66 INEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAAAK
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Adams M.D., Loftus B.J., Zhou L., Crosby M., Fuhrmann J., Mason T.M.,
Brandon R., Kim U.J., Kerlavage A.R., Venter J.C.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                    38 MNEE---LDKK---YAGLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPK
                                                                                                                                                                            ----SVEDISFDHSGKLLA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Johnstone R.W., Wang J., Tommerup N., Vissing H., Roberts T.,
"Ciao 1 is a novel WBdo protein that interacts with the tumor
suppressor protein WT1.";
J. Biol. Chem. 273:10880-10887(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
WD-repeat containing protein Ciao 1.
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124 SASEDATIKVWDYETGDFERTLKGHTD----
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076071;
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14; 65

Indels 141; Gaps

Matches 108; Conservative

Similarity

Query Match Best Local

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.X., Mizhy D.W., Sodergren B.J., Lu X., Glibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield X.W., Touchman J.W., Schmutz J., Myers R.M., Schlin J.E., Schmutz J., Myers R.M., Schlin J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PRINTS; PR00320; GPROTEINBRPT.
PYCODOM, PD000018, WD40; 2.
SMART; SM00320; WD40; 7.
PROSITE; PS00678; WD REPEATS 1; 1.
PROSITE; PS50082; WD_REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS REGION; 1.
Repeat; WD repeat; NUClear protein.
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289 WD
338 WD
37840 MW;
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Best Local Similarity 31.93
Matches 86; Conservative
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LGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDN----CVHDLQQHNK 392

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

August 9, 2004, 16:41:13 ; Search time 34.6667 Seconds (without alignments) 4678.164 Million cell updates/sec

Title: Perfect score) Sequence:

US-09-987-701-4
2718
1 MSISSDEVNFLVYRYLQESG.....LPHHLVVIPLVALIELLVLK 514

Scoring table:

1017041 segs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL\_25:\* Database :

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fung1:\*
sp\_fung1:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_organelle:\*
sp\_organelle:\* sp\_rvirus:\*
sp\_bacteriap:\* sp plant:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

# SUMMARIES

Description	08bhis musculus	SILE	SILE	xeno		mus	D mod		O9xzkl drosophila	Offile arabidopsis	095r19 drosophila	OBved3 mus musculu	O8z0rl anabaena sn	odospora		
Q	QBBHJS	O8CBG4	O9EOD4	Q7SZM9	QBBYQ4	Q8BMM0	Q86UY2	OBCOAL	Q9XZK1	09FN19	Q95RJ9	Q8VEG3	Q8ZOR1	08X1P3	08X1P5	Q8X1P4
DB	11	11	11	13	11	11	4	11	Ŋ	10	Ŋ	11	16	٣	m	m
% Query Match Length DB	514	514	514	519	527	527	577	412	700	613	524	201	1227	1356	1356	1356
% Query Match	90.8	90.7	90.7	89.1	83.6	83.5	82.0	64.8	63.1	46.0	34.0	32.5	16.4	16.3	16.3	15.9
Score	2468	2465	2464	2421.5	2273.5	2269.5	2229	1761.5	1715.5	1251	923.5	882	444.5	442	442	433.5
Result No.	П	7	m <sub>.</sub>	4,	Ŋ	v	7	89	σ	10	11	12	13	14	15	16

Q8y109 anabaena sp	Q8yzi2 anabaena sp	podospora	9 anabaena	anabaena		chizosaco	Osvens anabaena sn	ides omo	O96698 drosophila	OByse anabaena sp	mus musc	O8z054 anabaena sn	O8n776 homo sanien	0803d2 brachydanio		Osvtdl anabaena sp	xenopns ]	O9xbd8 amycolatons	O80990 arabidopsis		093531 xenopus lae	xenopns		mus	098hkl rhizobium l		Optr5 gallus gall	Q8ysc0 anabaena sp
QBYL09	Q8YZI2	Q8X1P2	082019	Q8YZ23	Q8Z020	074845	OBYMU3	Q8N136	096698	QBYSG6	Q9D4T2	Q8Z0E4	977N80	080302	074855	QSYTD1	Q90ZL4	Q9XBD8	066080	Q8YZ16	093531	Q7ZXK9	Q9DCZ7	Q99KN2	Q98HK1	Q9GL51	Q9PTR5	Q8YSC0
16	16		9	16	9		9		Ŋ	9	디		4	13	m	16		N		16	13	13	11	디	16	9	13	16
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15.8	15.7	15.6	15.0	14.9	14.5	14.1	14.0	13.8	13.6	13.6	13.6	13.6	13.5	13.5	13.5			13.2					13.0		12.9		12.9	12.7
• 1	426	423.5	408		395	382.5	381	376	370.5	369	368.5	368.5	368	367	366		60	357.5	356	354	53.	353.5	352	352	351.5	349.5	349.5	344.5
17	æ :	19	20	21	22	23	24	25	26	27	28	294	30	31	32	33	34	35	36	37	38	ტ ტ	40	41	42	43	44	45

## ALIGNMENTS

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X MEDLINE-2354645 TISSUE-Cerebellum,
X MEDLINE-23546681;
The FANTOM Consortium,
The FANTOM Consortium,
The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The Malysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
In Mature 420:563-573(2002).
R EMB:, AR035664; BAC29294.1;
R MGD; MGI:2441730; Iral.
R MGD; MGI:2441730; Iral.
R MGD; MGD:40650; MD40.
R Pfam; PF00400; WD40. 8.
R PRINTS; PR00120; GPROTEINBRPT.
R SWART; SW00667; Lish;
R SWART; SW00667; Lish;
R SWART; SW00667; Lish;
R SWART; SW00667; Lish;
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                                                                                                                                                                                                                                                                                                                               61 BAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAATNQ 120
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                                                                                                                                                                                                   1 MSISSDEVNPLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV 60
                                                                                                                                              1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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90.8%; Score 2468; DB 11; Length 514; 98.5%; Pred. No. 5e-167; trive 2; Mismatches 5; Indels 0.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS0678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
                                     Best Local Similarity 98.5
Matches 465; Conservative
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IRA1 OR 8030499H02RIK.
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Zhang X., Dornady S., Basch R.;
Identification of four human cDNAs that are differentially expressed
by eartopoietic progenitors.";
Submitted (MAY-2000) to the BMBL/GenBank/DDBJ databases.
REMBL; AP268195; AAG44738.1;
RMD; MG12441730; Iral.
RICEPRO; IPR006594; Lish.
RICEPRO; IPR006594; Lish.
REMBL; PR00400; WD40; B.
REMAT; SW00320; GPRCTEXNBRPT.
REMAT; SW00320; GPRCTEXNBRPT.
REMAT; SW00667; Lish; 1.
REMAT; SW00667; Lish; 1.
REMAT; SW00320; WD40; B.
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REMAT; SW00320; WD40; B.
REMAT; SW00320; WD40; B.
REMAT; SW00320; WD40; B.
REMAT; RW031E; PS05082; WD REPEATS_1; 4.
REMOSITE; PS05082; WD REPEATS_REGION; 1.
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                                                                                                                      1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV 60
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                                      Query Match 90.7%; Score 2465; DB 11; Length 514; Best Local Similarity 98.3%; Pred. No. 8.2e-167; Matches 464; Conservative 3; Mismatches 5; Indels 0;
514 AA; 55689 MW; 13BED3753A725029 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN-C57BL/6; TISSUB-Brain;

STRAIN-C57BL/6; TISSUB-Brain;

MEDLINE-2538825; PubMed=1247932;

MEDLINE-2538825; PubMed=1247932;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

RA Branchein M., Soares M.B., Bonaldo M.F., Caardinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

Roback S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Roback S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Rah, J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rah, Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                         HTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAI 355
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        EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAA-- 118
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STRAINE-257BL/60; TISSUE-Hypothalamus;
MEDLINE-22354683; PubMed=12466851;
The FANTOM CONSORtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
MADLINE-25156 of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                              AWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNS
                                                                                          ---SQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFIC
                                                                                                                  121 TPNNQQPPAKNGENTANGESNGGHALANNHTDMMEVDGDVEIPSSKAVVLRGHESEVFIC
                                                                                                                                                                                                                181 AWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNS
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Rodentia, Sclurognathi; Muridae, Murinae, Mus.
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Last sequence update)
Last annotation update)
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Mammalia; Eutheria;
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"Fusion Protein of Retinoic Acid Receptor {alpha} with Promyelocytic Leukemia Protein or Promyelocytic Leukemia Zinc Finger Protein Recruits N-CoR-TBLRI Corepressor Complex to Repress Transcription in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor co-repsor complex subunit TBLR1.
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                              Length 514;
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Pred. No. 1e-163;
                                                                                   Indels
6A72CE68A40C141F CRC64;
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                                           DB 11;
                                         Score 2464; DB 11
Pred. No. 9.6e-167
2; Mismatches 6
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EMBL; AY225088; AAP20646.1; -.
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  55689 MW;
                                       tch 90.7%; al Similarity 98.3%; 464; Conservative
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96.0%;
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514 AA;
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J. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 83.6%; Score 2273.5; DB 11; Length 527; Local Similarity 87.4%; Pred. No. 3.4e-153; Loss 425; Conservative 26; Mismatches 20; Indels 15;
                                                                                            | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Strains-27 | Str
                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
        cDNA sequences.";
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SEQUENCE FROM N.A.

C STRAIN=CSTBL/6J; TISSUE=Pituitary;

STRAIN=CSTBL/6J; TISSUE=Pituitary;

A The FANINCM Consortium,

The FANIOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

Thanlysis of the mouse transcriptome based on functional annotation of 60,770 full-length coDMs.";

In Mallysis of the mouse transcriptome based on functional annotation of Roll 1-1 ength coDMs.";

In Mature 420:563-573(2002).

In Mature 420:563-573(2002).

In REBL; AKO80147; EAC27015.1; -..

R PIR; PT0651; PT0651.

R InterPro; IPR006694; Lish.

R InterPro; IPR006694; Lish.

R Pfam; PF00400; WD40; R.
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.2%; Pred. No. 6.6e-153;
Matches 424; Conservative 26; Mismatches 21; Indels 15;
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ProDom; PD00018; WD40; 3.
SWART; SM00667; Lish; 1.
PROSITE; PS50896; LiSh; 1.
PROSITE; PS50896; LiSh; 1.
PROSITE; PS50089; WD REPEATS 1; 4.
PROSITE; PS50089; WD REPEATS 2; 6.
PROSITE; PS50089; WD REPEATS 2; 6.
SROUNCE 527 AA; 56832 MW; 0466F764ABA25CB0 CRC64;
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Mus musculus (Mouse)
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RESULT Q86UY2

(TremBlrel. 23, Created) (TremBlrel. 23, Last sequence update) (TremBlrel. 25, Last annotation update)

QBBMMO; 01-MAR-2003 ( 01-MAR-2003 ( 01-OCT-2003 ( Transducin.

PRELIMINARY;

Q8BMM0

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228 VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD
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(TrEMBLrel. 25, I
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Best Local Similarity
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01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                             408
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WA KIAUUNE=Z218825, PubMed=12477932,
WA KIAUUNE=Z218825, PubMed=12477932,
KIAUUNETER N.D. Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonado M.F., Casnanoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Du X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Monses S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 577;
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052304, AH522904.1;
InterPro; IPR005694; LisH.
InterPro; IPR005694; WD40.
Pfam; PF00400; WD40; 8
PRINTS, PR00320; WD40; 3
SMART; SM00567; LisH; 1.
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
SEQUENCE 577 AA; 62495 NW; D830A37781E2A1SC CRC64;
                                                                      Last sequence update)
Last annotation update)
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82.0%; Score 2229; DB 4;
Best Local Similarity 85.4%; Pred. No. 5.6e-150;
Matches 414; Conservative 32; Mismatches 25;
       577 AA
                                                     Created)
                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                             TBL1X protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Pancreas;
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291 VISLDWNINGTLLAIGSYDGFARIWTEDGNLASTLGQHKGPIFALKWNRKGNYILSAGVD
                                                                            288 KITIIWDAHIGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHYCKLGQDRPIKTFQG
                                                                                                                    351 KTTIIWDAHTGEAKQOPPHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTF0G
                                                                                                                                                                                             348 HINEVNAIKWDPIGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKBIYTIKWSPIGPGTN
                                                                                                                                                                                                                                  NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTOLVLRHCIREGGODVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 AQQQAAAAAAAAAAAQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVBIPPNKAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINB=225154683; PubMed=12466851;
The FANTOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the TANTOM CANAS.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 412;
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REMBL, AK031937; BA027612.1; -.

REMBL, AK031937; BA027612.1; -.

REMBL, PT0651; PT0651.

InterPro; IPR001680; WD40; WD40; RPRIMTS; PR00120; GPROTEINBRT.

REMINTS; PR001320; WD40; RPROSITE; PS00678; WD REPEATS 1; 4.

REMSITE; PS00678; WD REPEATS 1; 4.

REMSITE; PS0082; WD_REPEATS 2; 6.

REMSITE; PS0082; WD_REPEATS 2; 6.

REMSITE; PS0082; WD_REPEATS 2; 6.

REMOSITE; PS0082; WD_REPEATS 2; 6.

REMOSITE; PS0082; WD_REPEATS 2; 6.

REMOSITE; PS0082; WD_REPEATS 2; 6.

REMOSITE; PS0082; WD_REPEATS 2; 6.

REMOSITE; PS0082; WD_REPEATS 3; 6.

REMOSITE; PS0082; WD_REPEATS 3; 6.
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Last sequence update)
Last annotation update)
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64.8%; Score 1761.5; DB 11
Best Local Similarity 87.0%; Pred. No. 5.8e-117;
Matches 321; Conservative 20; Mismatches 27;
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61 EVEWSVGEDGEV--ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 -----OAYRDKLA----OOAAAAAAAAAAAAAAAAAAAAAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDÓSASEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AGGNQASTGGSNSTSTPAGGDLAAPCASOKKSONSNEAGSSSSGNAGNANATSTDDAASS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 -----REVDGDVEIPPNKAVVLRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 GNNVQSGSSNAQSSAPSGTISSSTSGGAGTPAALVPMDIDENIEIPESKARVLRGHESEV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 FICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSISSDEVNFLUYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRO-------96
                                                                                                                                                                                                                      Ceiniker S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R., Harris N.L., Aðbayani A., Arcaina T.T., Baxere E., Blazej R.G., Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J., Kim S.H., Lee B., Houston K.A., Hummasti S.R., Karra K., Karney L., Kim S.H., Lee B., Lomcoran M.A., Mak J., Maxda P., Moshrefi A.R., Moshrefi M., Nixon. K., Pacleb J.M., Park S., Peieffer B., Punch E., Snir E., Twomey B., Wan K.H., Zhang R., Zieran L.L., Rubin G.M., Solir E., Twomey B., Submitted (OCT-1998) to the EMBL, GenBank/DDBJ databases.

EMBL, AF146345, AAD35017.1;
                                                                                                   ebi regulates epidermal growth factor receptor signaling pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 63.1%; Score 1715.5; DB 5; Length 700; Best Local Similarity 52.9%; Pred. No. 2.33-113; Matches 71; Indels 191; Gaps Matches 349; Conservative 49; Mismatches 71; Indels 191; Gaps
                  SEQUENCE FROM N.A.
DEDLINE-99234084; PubMed=10215623;
DONG X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W.,
Zipursky S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGNIC PROGRESS OF PROTEINBRPT.
PRINTS; PRO0320; GPROTEINBRPT.
PRODOM; PRO0018; WD40; 3.
SMART; SM00667; LisH; 1.
SMART; SM006720; WD40; 8.
PROSITE; PS008037; MYB 1; 1.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS0062; WD_REPEATS_1; 3.
PROSITE; PS0062; WD_REPEATS_2; 6.
PROSITE; PS0062; WD_REPEATS_REGION; 1.
REPEAT; WD_REPEATS_REGION; 1.
SEQUENCE 700 AA; 72387 MW; 28C6DBB07BB79FB7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AC065762; -; NOT ANNOTATED_CDS.
FlyBase, FBGN0023444; ebi.
GC; GO:0000074; P:regulation of cell cycle; IMP.
InterPro; IPR004594; Lish.
InterPro; IPR004065; Myb DNA_binding.
InterPro; IPR001680; WD40.
                                                                                                                                           Genes Dev. 13:954-965(1999).
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                                                                                                                                                                                  SEQUENCE FROM N.A.
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233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292

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WDAHIGEAKQOFPFHSAPALDVDWQSNNIFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV 352
                                                                                                                       537
                                                                                                                                                                                           LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninoi P., Dale J.M., Goldsmith A.D., Haysshizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlih-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                    NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones.";

DNA Res. 4:401-414(1997).
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01-COT-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, Tac cloner(RAR14 (AT5967320/KBK14_4).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Youyen M., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H. Scker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98162728, PubMed-9501997,
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Arabidopsis ORF clones.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB007645; BAB09017.1; -.
EMBL; AY057698; AAL1532811; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       613
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InterPro; IRR006594; Lish.
InterPro; IPR001680; WD40.
Pfam; PR00400; WD40; 8.
PRINTS; PR00320; GPROTEINBRPT.
SWART; SM00657; Lish; 1.
SWART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 613;
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last annotation update)
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PROSITE; PS00896; LISH; 1.
PROSITE; PS0082; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
SEQUENCE 613 pa.
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NCBI_TaxID=7227;
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Best Local Similarity 99.4
Matches 158; Conservative
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NCBI TaxID=103690;
                                                                                                   SEQUENCE FROM N.A.
    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 14.0%; Score 923.5; DB 5; Length 524; Local Similarity 40.5%; Pred. No. 2.8e-57; Los 218; Conservative 39; Mismatches 64; Indels 217; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-WAR-2002 (TrEWBLrel. 20, Created)
01-WAR-2002 (TrEWBLrel. 20, Last sequence update)
01-MAR-2003 (TrEWBLrel. 20, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Similar to IRAI protein (Fregment).
Wus musculus (Mouse).
Eukaarjota: Metazoa (Dordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AYOGA326, AAL280874.1;
R Flybase; FBGN003344; ebi.
R GO: GO:0000074; P:regulation of cell cycle; IMP.
R InterPro; IPR00165; Mb40.
R InterPro; IPR001065; Mb40.
R InterPro; IPR001069; Mb40.
R PRINTS; PR00320; MB40.3.
R PRINTS; PR0030018; WD40.1.
R SWART; SM00667; Lish; 1.
R ROSITE; PS00037; MW10.3.
R PROSITE; PS00037; MW10.3.
R PROSITE; PS00037; MW10.3.
R PROSITE; PS00037; MW10.3.
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Natanabe A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T.,
Rishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Rishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
Complete genomic sequence of the filamentcus nitrogen-fixing
et cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 81205-713(201).
BRI, APR03581; BAB77553.1; -.
BRI, APR03581; BAB77553.1; -.
BRI, ARI810; ARI810.
CO, GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005525; P:tenscription factor activity; IEA.
GO; GO:0005525; P:tenscription factor activity; IEA.
GO; GO:0005355; P:tenscription factor activity; IEA.
RO; GO:0005355; P:tenscription factor activity; IEA.
RO; GO:0005355; P:tenscription of transcription, DNA-dependent; IEA.
RITHEPPO; IPR000797; HTH Fis.
RITHEPPO; IPR001982; HTH-LUXR.
RITHEPPO; IPR001882; MD40.
RITHEPPO; IPR001882; MD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 KIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKIFQGHTNEVNAIKWDPTGNLLASCSDDMTL
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.5%; Score 882; DB 11; Length 201; 99.4%; Pred. No. 6.5e-55; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 201 AA; 22038 MW; 6B945F137B491818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 CIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
WD-40 repeat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1227 AA.
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/D
EMBL, BC018512, AAH18512.1;
InterPro, IPR001680; WD40.
Pfam, PF00400; WD40, 4.
PRINTS; PR00320; GFROTEINBRPT.
ProDom; PD000018; WD40; 2.
SWART; SW00320; WD40; 4.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS00678; WD REPEATS 2; 3.
PROSITE; PS50082; WD REPEATS 2; 3.
PROSITE; PS5024; WD REPEATS 2; 3.
PROSITE; PS5024; WD REPEATS 2; 3.
PROSITE; PS5024; WD REPEATS 2; 3.
PROSITE; PS5024; WD REPEATS 3.
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MEDLINE=21595285; PubMed=11759840;
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repeat.
1356 AA; 149694 MW; 572A0B034DCE0D21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C.
                        PRINTS; PRO0320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
SWART; SM00320; WD40; 10.
SWART; SM00337; WACHT; 1.
PROSITE; PS500837; WD REPEATS_1; 10.
PROSITE; PS50082; WD REPEATS_2; 10.
PROSITE; PS50294; WD REPEATS_REGION; 1.
REPEATS_BEGUENCE 1356 AA; 149694 WW; 572A0B03.
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  Pfam; PF00400; WD40; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                       64 VSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQ-----QAYRDKLAQQQAAAAAAAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ASQQGSAK----NGE--NTANGEENGAHTIANNHTDMMEVDG-------DV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834 CGEDRSIKLWDIQRGECVNTLWGHSSQVWAIA-----FSPDGRTLISCSDDQTARLWDV 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        888 -ITGNSLNILRGYTRDVYSVAFSPDSQILASGRDDYTIGLMNLKTGEC---------HPL 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | | : : : : | : | : | : | : | R-GHQG-----RIRSVAEHPDGKILASGSADNTIKLMDISDTNHSKYIRTLTGHTNWVWT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 LKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 IHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQH 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 REGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIW----TKDGNLASTLGQHKGPIFA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 EIPPNKAVVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 NKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTK-HQEPVYSVA
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                   16.4%; Score 444.5; DB 16; Length 1227; 29.2%; Pred. No. 9.9e-23; ive 73; Mismatches 171; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
NCBI_TaxID=5145;
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"A new family of WD40 proteins implicated in vegetative incompatibility; evidence for a major role of WD40 repeat the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF323584; AAL37300.1;
InterPro; IPRO07111; NACHT_NTPase.
InterPro; IPRO07111; NACHT_NTPase.
PF05729; NACHT; 1.
                                                                                                                                                                                                                                                      1227 AA; 137236 MW; 466F726939ED4FBF CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*40.
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                PRINTS; PRO0364; DISEASERSIST.
PRINTS; PRO0320; GPROTEINBRFT.
PROM0320; WD40; 1.
SMART; SM00320; WD40; 14.
TIGREAMS; TIGRO1199; HTH fist; 1.
PROSITE; PS00678; WD REPENTS 1; 12.
PROSITE; PS50082; WD REPENTS 2; 14.
PROSITE; PS5024; WD REPENTS 2; 14.
PROSITE; PS10278; MD REPENTS 2; 14.
PROSITE; PS10278; WD REPENTS REGION; 1.
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1es 130; Conservative
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WD40; 14
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1180 VHSVAFSPDGQ-----RVASGSIDGTIKIWDAASGTCTQTLEGHGGWVHSVAFSPD 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                         163 VVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGS-TQLVLRHCIREGGQD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 ILSAGVDKITIIWDAHIGEAKQQFPFHSAPALDVDWQSNNTF-----ASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 CKLGQDRPIKTFQGHTNEVNAIKWDFTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD 453
                                                                                                                                                 56 GLQYVEA-----EVSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQA
                                                                                                                                                                                            109 AAAAAAAAAAQQGSAKNGE-----NTANGEENGAHTIANNHTDMMEVDGDVEIPPNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927 SVLSVAFSPDGQRVASGSGDKTIKIWDTASG--TGTQT--------
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"A new family of W040 proteins implicated in vegetative
incompatibility; evidence for a major role of W040 repeat domain in
the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF333582; AAL37298.1; -InterPro; IPR00711; NACHT_NTPase.
InterPro; IPR00160; W040.
Pfem; PF00400; W040: 10.
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Query Match
16.3%; Score 442; DB 3; Length 1356;
Best Local Similarity 27.6%; Pred. No. 1.7e-22;
Matches 130; Conservative 71; Mismatches 168; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
NCBL_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 GRYLASGSFDKCVHIW-------NTQVCL--HYLNGQVLLNLGR
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1009 ---GNSVMSVAFSPDGQRVASGSDDKTIKIWDTASGTCTQTLEGHGGWVWSVAFSPDGQR 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1066 VASGSIDGTIKIWDAASGTCTQTLEGHG-----DWVQSVAFSPDGQRVASGSDDHTIKI 1119
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                                                                                                                                                                                                                                        56 GLQYVEA-----EVSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQA 108
                                                                                                                                                                                                                                                                                                           109 AAAAAAAAASQQGSAKNGE-----NTANGEENGAHTIANNHTDMMEVDGDVEIPPNKA 162
                                                                                                                                                                                                                                                            163 VVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGS-TQLVLRHCIREGGQD
                                                                                                                                                                       Query Match
16.3%; Score 442; DB 3; Length 1356;
Best Local Similarity 27.6%; Pred. No. 1.7e-22;
Matches 130; Conservative 71; Mismatches 168; Indels 102; Gaps
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                                                                                                                                                                                                                                                                                                                                 1356 AA; 149720 MW; 9A80777304B361D0 CRC64;
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
SWART; SM00320; WD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS50087; WD_REPEATS_1; 10.
PROSITE; PS50082; WD_REPEATS_2; 10.
PROSITE; PS50084; WD_REPEATS_2; 10.
PROSITE; MD repeat.
SEQUENCE 1356 AA; 149720 MW; 9A8077730
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Search completed: August 9, 2004, 16:48:10 Job time: 47.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 9, 2004, 16:41:43; Search time 13.3333 Seconds (without alignments) 3708.183 Million cell updates/sec Run on:

US-09-987-701-12
2731
1 MSISSDEVNFLVYRYLQESG.....GDKVGASASDGSVCVLDLRK 514 Title: Perfect score: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	probable membrane	eat pro	ransducin-l		eat p	WD-40 repeat prote	repeat pro-	pea	L	-40	WD-40 repeat prote	WD repeat protein	nsđuc	hypothetical prote	WD-repeat protein	hypothetical prote	WD-repeat protein	trp-asp repeat con	WD-40 repeat prote	WD-repeat protein	hypothetical prote	serine/threonine k	WD-40 repeat-prote	8	tica	acti	cal pro	1 WD-r	1
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PF20 protein, micr WD-repeat protein	INFOLMETICAL PIOUE TATA box-binding p hypothetical prote hymothetical prote	WD-repeat protein MET30 protein - ye	hypothetical prote beta transducin-li WD-40 repeat regul	beta transducin-li transcription init transcription init hypothetical prote
T08180 AG2400	534023 T00798	AE2490 S49932 AI2099	T19266 T42045 T46032	S76414 S33263 T41454 T27513
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606 589 473	797 787 787	34.2 64.0 55.0 75.0	376 1049 317	1191 704 643 501
000	0000	O 10 4	444	4 W C1 H
227	idda	1444	111	11.4 11.3 11.2 11.1
328.5 328 327 5	32 32 5 325 5 525 5	3134	312 312 311.5	310 307.5 307 303.5
330	3 8 8 8 2 8 4 8	36	39 40 41	4 4 4 4 2 6 4 0

## ALIGNMENTS

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Albera transducin-like protein - Podospora anserina
C;Species: Podospora anserina
C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18521
R;Sauge, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
A;Title: A gene responsible for vegetative incompatibility in the fungus Podospora anseri
A;Reference number: 218944; MUID:96009891; PMID:7557402
1393 RLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLWNISSGECLYTLHGHI 1452
                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: L28125; NID: 9607002; PID: 9607003; PIDN: AAA85775.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.9%; Score 462; DB 2; Length 13
Best Local Similarity 27.3%; Pred. No. 3.4e-25;
Matches 121; Conservative 74; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                               A,Accession: T18521
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: 1NA
A,Residues: 1-1356 <8AU>
                                                                : | :: | :: | :: | 182
                                        484 GGIFEVCWNAAGDKVGASASDGSVCVLDLR
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820 ISTISVVEAEWNACTQT
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A,Gene: het-el
A,Introns: 761/3
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WD-2.2.7
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC2239
C;Accession: AC2239
C;Accession: AC2230
C;Accession: AC2230
C;Accession: AC2230
C;Accession: AC2230
N; Spimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B.
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; WUID:21592285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 -TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-1526 <KUR>
A,Experimental source: GB:BA000019, PIDN:BAB75165.1; PID:g17132599; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr3466
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                                                                                                                                                                                                                                                                                                                                 ---VHSYRGTGGIFEVC 490
                                                                                                                                                                                                                                                                                                                                                                   454 GQKYAVAFMDGQVNVYDLKKLNSKSRSLYGNRDGILNPLPIPLYASYQSSQDNDYIFDLS 513
                          TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDK 200
                                                                                                      ----HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                              284 VIILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV 343
                                                                                                                                                                              334 CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
                                                                                                                                                                                                      344 YQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSFYGHSQS 403
                                                                                                                                                                                                                                                        394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD 453
                                                                                                                                                                                                                                                                                       404 IVSASWV------GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVPIFAGRISQD 453
                                                  TCLAWSHDGNSIVTGVENGELELWNKTGALLNVLNFHRAPIVSVKWNKDGTHIISMDVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 NGAHTIANNHTDMMEVDGDVEIPSNKAV-VLRGHESEVFICAMNPVSDLLVSGSGDSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWNLSENSTSGPTQLVLRHC--IREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIW
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llarity 30.3%; Pred. No. 1.7e-26;
Conservative 77; Mismatches 149; Indels 4
                                                                                                                                                                                                                                                                                                                                   454 GRYLASGSFDKCVHIW----NTQTGAL----
                                                                                                                                                                                                                                                                                                                                                                                                               WNAAGDKVGA--SASDGSVCVL 510
                                                                                                          TTIIWDAHTGEAKQQFPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 WNCAGNKISVAYSLQEGSVVAI
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Matches 118; Conserv
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A12155
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Dostoc sp. PCC 7120
C;Species: Ostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12155
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHGG 1010
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                                                          130
                                                                                                                    870
                                                                                                                                                                            ANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAMNPVSDLLVSGSGD 190
                                                                                                                                                                                                                                                                                                                                                           905 KTIKİMDAASGTC---TQTLEGH----GGR-----VQSVAFSPDGQRVASGSDDHTIK 950
                                                                                                                                                                                                                                                                                                                                                                                                                            IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                      310 PALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWD
                                                       IESLSLIDBAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAATNQQGSAKNGE-----NT
                                                                                                                    ----LEGHGSSVLSVAFSADGORVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                       191 STARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFAR
   Gaps
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RESULT 6
ALIBIO
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Accession: Azi810
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C; Accession: Azi810
C; Accession: Azi810
C; Accession: Azi810
C; Accession: Azi810
C; Accession: Azi810
C; Accession: Billion C; Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Reference number: AB1807; MUD:21595285; PMID:11759840
A; Reference number: AB1807; MUD:21595285; PMID:11759840
A; Residues: 1-1227 < KUR>
A; Residues: 1-1227 < KUR>
C; Genetics: 1-1227 < KUR>
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C; Genetics: 1-1227 < KUR
                                                                                      .441 TLIGHDNEVNKVNFSPDGKTLASASRDNTVKLMNVSDGKFKKTLKGHTDEVFWVSFSPDG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
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                        244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFPERSAPALDVDWO-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
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16.0%; Score 437; DB 2; Length 12;
Best Local Similarity 31.7%; Pred. No. 1.9e-23;
Matches 102; Conservative 61; Mismatches 129; Indels
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Reference number: AISI55
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1288 «KUR»
A;Residues: 1-1288 «KUR»
A;Experimental source: strain PCC 7120
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Geneti
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R;Accession: AF2071
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tasuda, M.; Tabata, A.;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21592585; MMID:11759840
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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
WD-50 repeat protein [imported] - Nostoc sp. (strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2071
V. WIN C. P.: Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule: 1-1683 «KUR»
A; Cross-references: GB: BA00019; PIDN: BAB73823.1; PID: g17131215; GSPDB: GN00179
A; Experimental source: strain PCC 7120
C; Genetics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1020 -----TDWVYAVVFHPOGKIIATGSADCTVKLWNISTGQCLKTLSEHSDKILGMAWSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
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Pred. No. 2.9e-24;
1; Mismatches 163,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1074 GOLLASASADOSVRLWD------
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Best Local Similarity 28.5%
Matches 109; Conservative
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7

Gaps

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Gaps

41;

Length 1708;

350

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EVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPN 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1461 LWH-QDGKILHTLQGHQDAVLAVAWSSDSQVIASAGKDKIVKIWSQG-GQLLHTLQGHTD
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                                                                                                                                                                                                                                                                1298 NRQG---NLLKTLSGHTAGVTAVTFSPNGETIGSASIDATLKLWSPQGLLLGTLKGHNSW
                                                                                                                                                                                                                                                                                                                                           172 VFICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 DWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWDAHIGEAKQOFPFHSAPALDVDWQSNN-TFASCSTDMCIHVCKLGQDRPIKTFQGHTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 TOTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDL 512
                                       Query Match
16.0%; Score 436.5; DB 2;
Best Local Similarity 30.5%; Pred. No. 3.3e-23;
Matches 123; Conservative 70; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1866
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A;Accession: AE1866
A;Accession: AE1807; MUD:21595285; PMID:11759840
A;Accession: AE1808
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A;A
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C, Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C, Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C, Accession: A12493 R, Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Irriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 205-213, 2001 A; Pittle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: A31807; MUID:21595285; PMID:11759840
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О
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A;Cross-references: GB:BA000020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 LASTLGOHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDV--D 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 ASGSFDQNVKLWDIHTGKCVWTLQGHTGVVTSVAFNPKDNLLLSGSYDQSVKVWDKKTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 CSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GHESEVFICAWNPVSDLLVSGSGDSTARIWNLSE----NSTSGPTQLVLRHCIREGGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- DVPSNK------DVTSLDWNSEGTLLATGSYDGFARIW-TKDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WQSNNTFASCSTDMCIHVCKLG------QDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSADRTIKLWSPHTGQCLHTLHGHGSWVWAIAFSLD------DKLLASGSYDHTVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.0%; Score 436.5; DB 2; 28.7%; Pred. No. 2e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 FEVCWNAAGDKVGASA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.71
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 -----
                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: A12493
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: alr/1127
A;Genome: plasmid
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C;Accession: AD1842
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complere Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1323 GRLIATASADKTITLWSRDGN-----IL-----GTFAGHNHEVNSLSFSPDGNIL 1367
                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1711 <KUR>
A;Cross-references: GB:BA00019; PIDN:BAB77808.1; PID:g17135262; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PSHTKOVLAVTFSPDG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTIVSAG------ADNTVKLWSRNGTL-----LTTLEGHNEAVWQVIFSPD 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINEDGTL----FDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAATNQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 415; DB 2; Length 1711; 24.9%; Pred. No. 1.2e-21; ive 75; Mismatches 180; Indels 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match, 15.2%,
Best Local Similarity 24.9%,
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1246
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A;Residues: 11708 «KUR»
A;Cross-references: GB:BA00019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:

C,Genetics: A,Gene: all0478

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MOT889
WD-40 repeat protein (imported] - Nostoc sp. (strain PCC 7120)
ACT889
WD-40 repeat protein (imported] - Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1889
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
NAR Res. 8, 205-213, 2001
A;Reference number: A31807; MUID:2159285; PMID:11759840
A;Accession: AG1889
A;Status: preliminary
A;Residues: 1-934 eKURs.
A;Residues: 1-934 eKURs.
A;Residues: 1-934 eKURs.
A;Residues: 1-934 eKURs.
A;Accession: AG1889
A;Residues: DNA
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A,Experimental source: strain PCC 7120
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   EDGTLFD---GRPIESLSLIDA-VMPDVVQTRQQAY----RDKLAQQHAAAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQQGSAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPSNKAVVLRGHESEVF-ICAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 SEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDSQLLATASWDNTVKLWSREGKLLHTLEGHKDKVNSITFSPDGQLIATVGWDNTMKLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 AHTGEAKQOFPFHSAPALDVDWQ----SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 L-DGKELRTFRGHQ----DMIWSVSFSPDGKQIATASGDRTVKLWSL-DGKELQTLRGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 HILIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 VNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVEAEVSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 ISSLVTGLILALGLAGVAWLQGQKARMSETK------AISSSAESFLNANLEF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQ--DVPSNKD-VTSLDWN
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Best Local Similarity 23.1%; Pred. No. 3.5e-21;
Matches 128; Conservative 115; Mismatches 197; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T40883
WD repeat protein - fission yeast (Schizosaccharomyces pombe)
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A;Gene: all0664
                                       1659
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AC1842
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. Strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Accession: AC1842

B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUD:21595285; PMID:11759840

A;Accession: AC1842

A;Accession: AC1842

A;Molecule type: DNA
                                                                                                                                                                                                                       1488 QILASGSADKTIKLMSV-NGRLIKTLIGHNGWYTDIKFSADGKNIVSASADKTIKINSL- 1545
                                                                                                                                                                                                                                                                                                                                                                          1595
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1368 ASGSDDNTVRLWTVNRTLPKTFYGHKGSVSYVRFSNDGKKITSLSTDSTMKTWSLDGKLL 1427
                                                                                                                        1428 QTLSSPLPDVTSISFTPDNKIVALASPDHTIHLYNRQGGLLRSLPGHNHWITSLSFSPNK 1487
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LTGHKERITSVKFSPDGKILASASGDKTIKFWNTDGKFLKTIAAHNQQVNSINFSSDSKT 1369
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                                                                                                                                                                                                                                                                                                            380 QDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLT 439
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A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                   1546 DGRLIRTLQGHSASVWSVNLSPDGQ-----TLASTSQDETIKLWNLN-GELLYTLR
                                                                                                                                                                                320 NTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMK
                                                                                                                                                                                                                                                                                                                                                                                                                              440 KHQEPUYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKV
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                                                                 --HT-----GEAKQQFPFHSAPALDVDWQSN-
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N;Alternate names: protein sll0163
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C;Accession: S76086
S;Xotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-564 <WOO>
A;Cross-references: EMBL:AL031764; PIDN:CRA21113.1; GSPDB:GN00068; SPDB:SPCC1235.09
A;Cross-references: EMBL:AL031764; PIDN:CRA21113.1; GSPDB:GN00068; SPDB:SPCC1235.09
A;Experimental source: strain 972h-; cosmid c1235
G;Genetics:
A;Gene: SPDB:SPCC1235.09
A;Gene: SPDB:SPCC1235.03
A;Map position: 3
A;Map position: 3
A;Introns: 18/1; 273/3; 413/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 LASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VELEKHYVDNHSSNEEASKTSIDGE----SLVNENPCKLPFYLTVPHICETTLTKADST 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 TGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40683
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: 221954
A;Reference number: 221954
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                                                                                                                                                                                                                                                                                                                                                Length 564;
                                                                                                                                                                                                                                                                                                                                           Query Match
14.3%; Score 391.5; DB 2;
Best Local Similarity 24.7%; Pred. No. 1.3e-20;
Matches 134; Conservative 106; Mismatches 201;
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hypothetical protein alr3119 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision-14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2195
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watenabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                   NID:g1001396; PIDN:BAA10064.1; PID:d101071:
to the EMBL Data Library, June 1996
WD repeat homology
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A;Molecule type: DNA
A;Residues: 1-676 «KUR»
A;Residues: GB:BA000019; PIDN:BAB74818.1; PID:g17132214; GSPDB:GN00179
A;Cross-references: GB:BA000019; PIDN:BAB74818.1; PID:g17132214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 RDKLAQQHAAAAAAAATNQQGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDKTARLWTTEGECVAVLADHQGWVREGQFSPDGQWIVTGS---ADKTAQLWNVLG----
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A, Title: Sequence analysis of the genome of the unicellular
                                                                                            A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.3%; Score 390.5; DB 2;
Best Local Similarity 28.5%; Pred. No. 7.2e-20;
Matches 107; Conservative 53; Mismatches 137;
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                                                                                                                                            A;Accession: S76086
A;Status: nucleic acid sequence not shown;
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                                                                                   953 QAWVRSVS-----FSRDGQYILTASDDCTARLWN----
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(Species Nostoc Sp. 100 (Strain PCC 7120)

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(Species Nostoc Sp. PCC 7120

(Species Nostoc Sp. Strain PCC 7120

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A;Cross-references: GB:BA000019; PIDN:BAB76533.1; PID:g17133971; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                              14.1%; Score 385.5; DB 2; Length 676; 24.2%; Pred. No. 4.6e-20; ive 82; Mismatches 191; Indels 125;
                                                                                                                                                                                                                             21 FSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVEA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3119
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Best Local Similarity 22.3%
Matches 120; Conservative
                                                                                                                                         Best Local Similarity 24.23
Matches 127; Conservative
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Q9EQD4
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Q9EQD4
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Q9xxk1 drosophila
Q9fn19 arabidopsis
Q8veg3 mus musculu
Q95rj9 drosophila
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Q7szm9 xenopus lae
Q8byq4 mus musculu
Q8bmm0 mus musculu
Q86uy2 homo sapien
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Q8bhj5 mus musculu
                                                                                                                                                                                                                  August 9, 2004, 16:41:13 ; Search time 34.6667 Seconds (without alignments) 4678.164 Million cell updates/sec
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Q8x1p5 podospora a
Q8x1p3 podospora a
Q8x1p2 podospora a
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2731
1 MSISSDEVNPLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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1: Sp_archea:*
2: Sp_bacteria:*
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Q8EBU5
Q8EBU5
Q8EBU9
QBENYQ4
Q8COA1
Q9COA1
Q9FN19
Q9FN19
Q9FN19
Q8VEG3
Q8VEG3
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sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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sp_virus:*
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Match Length
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Perfect score:
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24665.5
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1101
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No.
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O80990 arabidopsis	080990	10	352		355	
7	Q99KN2	11	339	13.0	355	44
mus	Q9DCZ7	11	339		355	
xenc	Q7ZXK9	m	476	•	357	
O93531 xenopus lae	093531		476		357	41
dictyoste	Q861S4		478		358	40
096995 drosophila	966960		480		28	99
mycolator	Q9XBD8		1241		361.5	38
Q8yz16 anabaena sp	Q8YZ16	16	265		36	37
096698 drosophila	869960	Ŋ	411		365	36
rosophil	Q8T4A2		488		66.	35
lrosophile	Q9VPR4		481		366.5	34
Q8z054 anabaena sp	Q8Z054	9	304		. 99	33
Q9d4t2 mus musculu	Q9D4T2	ы	304	13.4		32
Q8n776 homo sapien	977NBQ		415			31
074855 schizosacch	074855		502			30
Q8tmx4 methanosarc	Q8TMX4	-	1233			29
Q98hk1 rhizobium 1	Q98HK1	9	1430		370.5	28
Q8ytd1 anabaena sp	QRYTD1	ø	1189	13.7		27
Q8n136 homo sapien	Q8N136		415		376	26
O8ymu3 anabaena sp	QBYMU3	16	1551		385	25
Q8ysg6 anabaena sp	OBYSG6	ø	676		82	24
074845 schizosacch	074845		564	14.3	391.5	23
nabaena	Q8YZ23	9	934		03.	22
nabaena	Q8Z0Z0	9	1747		04.	21
nabaena	Q8Z019	ø	1711		Н	20
ınabaena	QBYZIZ	ø	1708		9	ц 9
anabaena	QBYL09	9	1189	16.0	36	18
Q8z0rl anabaena sp	QBZOR1	16	1227		437	17

## ALIGNMENTS

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Zhang X., Dormady S., Basch R.; "Identification of four human cDNAs that are differentially expressed
                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Description 100.0%; Score 2731; DB 11; Length 514;

Best Local Similarity 100.0%; Pred. No. 1.7e-184;

Matches 514; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by early hematopoietic progenitors.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268195; AAG44738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55689 MW; 6A72CE68A40C141F CRC64;
                                                                                                  Last sequence update)
Last annotation update)
   Ā
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InterPro; IPR006594; Lish.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
PRINTS; PF00400; WD40; 8.
SWART; SW00667; Lish; 1.
SWART; SW00667; Lish; 1.
PROSITE; PS00896; Lish; 1.
PROSITE; PS00678; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
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PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50087; WD REPEATS_1; 4.
PROSITE; PS50084; WD REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 514 AA; 55689 MW; 6A72CE68A40
                                                                  Created)
PRT;
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16,
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PRELIMINARY;
                               Q9EQD4;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:2441730; Iral.
                                                                                                                                                                                                    IRA1 OR 8030499H02RIK.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxiD=10090;
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Gaps

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08X1P5 08X1P3 08X1P2

us-09-987-701-12.rspt

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301
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SEQUENCE FROM N.A.
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SEQUENCE STRAIN-C57BL/G4; TISSUB=Testis;
X MEDLINE=2234683; PubMed=1246685;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SMART; SMO0320; WD40; B.
PROSITE; PS50896; LISH; 1.
PROSITE; PS00678; WD_REPEATS_1; 4.
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MEDLINE=2534689; PubMed=12466831;
The FANTOM Consortium,
The FANTOM Consortium,
The FANTOM Consortium,
The RIKIN Genome Exploration Research Group Phase I & II Team;
Thanlyais of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:653-573(2002).
PIR; PT0651; PT0651.
MOD; MG1:2441730; Ira1.
InterPro; IPR06594; LisH.
InterPro; IPR06594; LisH.
InterPro; IPR061680; WD40.
Pfam; PF00400; WD40; 8.
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Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                            ·;
                                                                                              Length 514;
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PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
SEQUENCE 514 AA; $5661 MW; 13BECIC2C7F8BF14 CRC64;
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                                                                                           99.9%; Score 2727; DB 11; 99.8%; Pred. No. 3.2e-184; ive 0; Mismatches 1;
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Best Local Similarity 99.8
Matches 513; Conservative
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STRAIN=C57BL/6J; TISSUE=Hypothalamus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                            DB 13; Length 519;
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STRAIN=CS7BL/6; TISSUE=Brain;
MEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Faingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
                                                                                                                                                                                                         Indels
                                                                              CRC64;
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Last annotation update)
                                                                                                                                     Score 2645.5; DB 13
Pred. No. 1.9e-178;
2; Mismatches 12;
                                                                              5E998EDC8C892296
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                                                                                                                                            96.9%;
96.3%;
             EMBL; AY225088; AAP20646.1;
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TBL1X.
                                                                                                                                        Query Match
Best Local Similarity 96.3
Matches 500; Conservative
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"Fusion Procein of Retinoic Acid Receptor (alpha) with Promyelocytic
Leukemia Protein or Promyelocytic Leukemia Zinc Finger Protein
Recruits N-CoR-TBLRI Corepressor Complex to Repress Transcription in
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Nuclear receptor co-repressor complex subunit TBLR1.
Xenopus laevis (African clawed frog).
Mararyota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Ambra, Mesobatrachia, Pipoidea, Pipidae;
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0
                                                                                                                                                                                                                                                                                                                                     Length 514;
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PRINTS; PR00320; GPROTEINBRPT.

ProDom; PD000018; WD40; 3.

SMART; SM00670; Liss; 1.

SMART; SM00320; WD40; 8.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50082; WD REPEATS 1; 4.

PROSITE; PS50294; WD REPEATS 2; 6.

PROSITE; PS50294; WD REPEATS REGION; 1.

SEQUENCE 514 AA; 55689 MW; 13BED3753A725029, CRC64;
                                                                                                                                                                                                                                                                                                                                 Score 2724; DB 11;
Pred. No. 5.3e-184;
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Best Local Similarity 99.69
Matches 512; Conservative
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NCBI_TaxID=8355;
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
than lyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:653-573 (2002).
ENBL; AK03047; BAC27015.1; -.
PIR; PT0651; PT0651.
MGJ; MGJ; MGJ; MGG594; LisH.
InterPro; IPR006594; LisH.
InterPro; IPR00660; W400.
PFam; PR00400; W400; W300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 527;
                                                                                              514
                                                                                                                                 480 HIWNTQSGSLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 527
                                                                                              467 HIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
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PRODOM; PD000018; WD40; 3.
SMART; SM00667; Lish; 1.
SMART; SM00520; WD40; 8.
PROSITE; PS50896; LISH; 1.
PROSITE; PS50895; WD REPEATS 1; 4.
PROSITE; PS50094; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS REGION; 1.
SEQUENCE 527 AA; 56832 MW; 0466F764ABA25CB0 CRC64;
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Last annotation update)
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Best Local Similarity 97.5%; Pred. No. 1.6e-165;
Matches 462; Conservative 27; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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   61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ--HAAAAAAAAAA 118
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Strauberg R.;
Strauberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK038674; BAC30092.1; --
EMBL; AK038674; BAC30092.1; --
PTR; PF0651; PF0651.
PTR; PF06651; PF06594; Lish.
InterPro; IPR006594; Lish.
InterPro; IPR00689; Wa40.
PRINTS; PR00320; GPROTEINBRPT.
PF050m; PF004001; Wa40. 8.
PRINTS; SM00667; Lish; I.
SMART; SM00520; WD40; 8.
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50092; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS REGION; 1.
SEQUENCE 527 AA; 56802 NW; 146435A9C51DFDA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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  GHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGT
                                                                                 407 NNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCV
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86.0%; Pred. No. 8.2e-164;
Live 33; Mismatches 27; Indels 14
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC052304; AAH52304.1; -.
REMBL, BC052304; AAH52304.1; -.
RINTERPOO; IPR001689; WD40.
R PRIMT; PR001400; WD40.8.
R PRIMTS; PR00180; WD40; 3.
R SWART; SM00320; WD40; 3.
R SWART; SM00320; WD40; 3.
R PROSITE; PS50896; LISH; 1.
R PROSITE; PS50082; WD REPEATS 1; 4.
R PROSITE; PS50082; WD REPEATS 1; 4.
R PROSITE; PS50082; WD REPEATS 2; 6.
R PROSITE; PS50082; WD REPEATS REGION; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity Matches 453; Conserv

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MEDLINE=223546893; PubMed=12466851;
The FANTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                52 MSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPAALISILQKGLQYV
                                                                                                                                     231 HESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKD
                                                                                                                                                                                                                                                                                                                                                                                                                                            471 NPNSNIMLASASFDSTVRLMDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVH
                                                                                                                     -----NOOGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRG
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1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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                                                           EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAT-
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
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Last annotation update)
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01-MAR-2003 (
01-MAR-2003 (
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MEDINE-20196006; PubMed=10731132;

MEDINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holmer B.W., Hoskins R.A., Galle R.F.,

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Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Change M., Pfeiffer B.D.,

ADAIL J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

Ballew R.W., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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R. Bosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

A Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Helman T.J., Wennandez J.R., Houck J.,

Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A.,

Kallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

Kalmmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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Bukaryota; Mecazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    Length 412;
                                                 Indels
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Last annotation update)
71.6%; Score 1956; DB 11;
87.1%; Pred. No. 6.4e-130;
ative 21; Mismatches 26;
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
                                                 Matches 359; Conservative
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    Query Mátch
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EBI OR CG4063.
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A nelson D.R., Stenster M.S., Panlard J., Puri V., Reese M.G.,
Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
She B.C., Siden-Krämos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Xao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.,
A Gibbs R.A., Myers E.W., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
B Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
B Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
B Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
B Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
B Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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EMBL; AC05762; -, NOT ANNOTATED_CDS.

RMBL; AC05762; -, NOT ANNOTATED_CDS.

RMBL; AC05762; -, NOT ANNOTATED_CDS.

ROJ, GO:0000074; P:regulation of cell cycle; IMP.

ROJ, GO:0000074; P:regulation of cell cycle; IMP.

InterPro; IPR001659; Myb_DNA_binding.

InterPro; IPR001659; Myb_DNA_binding.

InterPro; IPR001605; Myb_DNA_binding.
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MEDLINE-99234084; PubMed=10215623;
Dong X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W.,
Zipursky S.L.;
"ebi regulates epidermal growth factor receptor signaling pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
69.8%; Score 1906.5; DB 5; Length 700;
Best Local Similarity 54.8%; Pred. No. 4.2e-126;
Matches 385; Conservative 49; Mismatches 77; Indels 191; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEPERAL; WD repeat.
SEOUENCE 700 AA; 72387 MW; 28C6D8D07BB79FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0678; WIERPEATS 1; 3.
PROSITE; PS50082; WD_REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ANGEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PROGSZO; GPROTEINBRPT.
PPRODON; PD0000018; WD40; 3.
SMART; SMOG67; LisH; 1.
SMART; SMOG320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Dev. 13:954-965(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50896; LISH; 1.
PROSITE; PS00037; MYB_1; 1
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63 MEANLSNSEVDIDEDFSFF--QPLDLISKDVKELQDMLREKKRKEREDMEKERDK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 DIVMTPTSQTSHIPNSDVRILEGHTSEVCACAMSPSASLLASGSGDATARIWSIPEGSFK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 ASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------IPSNKAVVLRGHESEVFICAWNPVSDLLVSGSGDSTARIWNLSENSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 ISTLSKHKGPIFSLKMNKKGDYLLTGSVDRTAVVWDVKAEBWKQQFEFHSGPTLDVDWRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SLTSVELNFLVFRYLQESGFTHAAFTLGYEAGINKSNIDGNMVPPGALIKFVQKGLQYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GP----TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 NNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVE
Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H., Yu G., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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                                                                                                                                                                                                              "Arabidopsis ORF clones.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR007645; BAB09017.1; -.
EMBL; AY087698; AAL15328.1; -.
EMBL; AY143932; AAN28871.1; -.
InterPro; IPR0016594; LisH.
InterPro; IPR001680; WD40.
Pfont; PF001400; WD40; 8.
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PROSITE; PSS00678; WD_REPEATS_1; 3.
PROSITE; PSS0082; WD_REPEATS_2; 6.
PROSITE; PSS0294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 FIGURE, FROUGEON WARDS B.
PRINTS, PRO0320, GPROTEINBRPT.
ProDom, PD000018; WD40; 2.
SWART; SM00667; Lish; 1.
SWART; SM00320; WD40; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 NHTDMMEVD-----
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Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2] SEQUENCE FROM N.A. C.J., Koesema E., Meyers M.C., Banh J., Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Cheuk R., Carninci P., Dale J.M., Goldsmith A.D., Hayashlzaki Y., Bowser L., Carninci P., Dale J.M., Kallin-Neumann G., Ishida J., Lam B., Lee J.M., Lin J., Liu S.X., Mirzanda M., Narusaka M., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Quach H.L., Sakurai T., Squow M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                  AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS
                                                                                                                                FICAWNPSRDLLASGSGDSTARIWDMSDANTNS-NQLVLRHCIQKGGAEVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                     WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII
                                                                                                                                                                                                                                                                                                                                                                                                                                  WNCDGSLLATGSYDGYARIWKTDGRLASTLGQHKGPIFALKWNKCGNYILSAGVDKTTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAIKWDFTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSFTGPGTNNPNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
                                                                                                                                                                                               -----MEVDGDVEIPSNKAVVLRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 WDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CRT-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, TAC clone:K8K14 (AT5g67320/K8K14_4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGQLVHSYKGTGGIFEVCWNSKGTKVGASASDGSVFVLDLRK 699
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 TGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                               ----AHTIANNHTDM-----
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SEQUENCE FROM N.A.
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Gaps

108;

61 62 498 597

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Best Local Similarity 40.38 Matches 217; Conservative
                                                                                                                                                                   PROSITE; PS50896; LISH; 1. PROSITE; PS00037; MYB 1; 1
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Podospora anserina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NG----
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Q8X1P4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                          314 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KINSWKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANL/MLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 KIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to IRAl protein (Fragment).
Bukar musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                            Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                            SECURICE FROM N.A.
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC108512; AAH18512.1;
InterPro; IFR01680; WD40.
Pfam; PF00400; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                    201 AA; 22038 MW; 6B945F137B491818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.3%; Score 1101; DB 11;
Best Local Similarity 99.5%; Pred. No. 5.4e-70;
Matches 200; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 AA
                                                            201 AA
                                                                                                                                                                                                                                                                                            SMART; SM00320; WD40; 4.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS50082; WD_REPEATS 2; 3.
PROSITE; PS50224; WD_REPEATS REGION; 1.
Repeat; WD repeat.
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01-DEC-2001 (TrEMBLrel. 19, Last seqn
01-OCT-2003 (TrEMBLrel. 25, Last anno
                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGDKVGASASDGSVCVLDLRK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                    PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
 598 AACFADNSVCVLDFR
                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                       NCBI_TaxID=10090;
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EBI OR CG4063.
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                                                            Q8VEG3
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095RJ9
                                     RESULT 11
                                                  Q8VEG3
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61 EVEWSVGEDGEV--ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------QAYRDKIA------QHAAAAAAAAAAAATNQQGSAKNGENT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDQSASEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------MEVDGDVEIPSNKAVVLRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 WDASTG-----PMHPAICL----SQCSSLGCGLADKPGLCLLQYGSADTCVPVGCK 524
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Phouanenavong
                          Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY061326; AAL28874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50082; WD_REPEATS_2; 3.
PROSITE; PS50284; WD_REPEATS_2; 3.
REPORT: WD_repeat.
SEQUENCE 524 AA, 52529 MW; GC3D86110BA18D65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ANGEE----------
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(MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.7%; Score 920.5; DB 5;
40.3%; Pred. No. 1.2e-56;
live 37; Mismatches 67;
                                                                                                           FlyBase, FBgn002344; ebi.
GO; GO:000074; P:regulation of cell cycle; IMP.
InterPro; IPR001659; LisH.
InterPro; IPR001605; Myb DNA_binding.
InterPro; IPR001609; Wb40.
Pfam; PF00400; WD40; 3.
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  Nunoo J., Pacleb J., Paragas V., Park S.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.
                                                                                                                                                                                                                                                                                  PRINTS; PR00320; GPRCTEINBRPT.
PRODON: PD000018; MP40; 1.
SMART; SM00657; LieH; 1.
SMART; SM00320; WD40; 3.
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Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora
                                                                                                                                                                                                                                  SMART; SM00320; WD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS50837; NACHT; 1; 10.
PROSITE; PS5082; WD_REPEATS_1; 10.
PROSITE; PS50824; WD_REPEATS_2; 10.
Repeat; WD_repeat.
SEQUENCE 1356 A4; 149720 MW; 9A80777
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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               NCBI_TaxID=5145,
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Matches
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Q8X1P3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 IWDAHTGEAKQQFPFHSAPALDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                      78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAATNQQGSAKNGE-----NT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ANGEENGAHTIANNHIDMMEV----DGD-VEIPSNKAVV------LRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 ISTISVVEÅEWNACTQT-----LEGHGSSVLSVAFSPDGQRVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 FICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1035 IWDTASGTCTQTLEGHGG-----WVQSVAFSPDGQRVASGSNDHTIKIWDAASGTCTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 FQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGP
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                      SEQUENCE FROM N.A.

Espagne E., Balhadere P., Begueret J., Turcq B.;

"A new family of WD40 proteins implicated in vegetative
incompatibility; evidence for a major role of WD40 repeat domain in
the specificity of het-e and het-d genes.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF323583, AAL37299.1; -.

InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1200 TIKIWDAASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSSDNTIKIWD 1247
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVHIWNTQTGALVHSYRGTGG-IFEVCWNAAGDKVGASASDGSVCVLD 511
                                                                                                                                                                                                                                                                                                                                                                         17.6%; Score 480; DB 3; Length 1356; 27.8%; Pred. No. 5.5e-25; ive 78; Mismatches 186; Indels 7
                                                                                                                                                                                     Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
PRINTS; PRO0320; MACHT; 1.
ProDom; PRO811E; PS5081; MACHT; 1.
PROSITE; PS5082; WD_REPEATS 1; 10.
PROSITE; PS5024; WD_REPEATS 2; 10.
PROSITE; PS5024; WD_REPEATS 2; 10.
PROSITE; PS5024; WD_REPEATS 2; 10.
PROSITE; PS5024; WD_REPEATS 2; 10.
PROSITE; PS6082; MACHT; 1.
PROFITE; PS5024; MACHT; 1.
PROFITE; PS5024; WD_REPEATS 3148AF4A7B82826 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C.
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Best Local Similarity 27.84
Matches 130; Conservative
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1035 IMDTASGTCTQTLEGHGGWVWSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGD 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            975 FSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHGNSVWSVAFSPDGQRVASGSDDKTIK 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWDAHTGEAKQOFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       871 ASG--TGTQTLEGHGGSVWSVAFSPDGQRVASGSDDKTIKIWDAASGTCTQTLEGHGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 FICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 WNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAATNQQGSAKNGE-----NT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
Espagne E., Balhadere P., Begueret J., Turcq B.;

Espagne E., Balhadere P., Begueret J., Turcq B.;

I ncompatibility evidence for a major role of WD40 repeat dome incompatibility; evidence for a major role of WD40 repeat dome the specificity of het-e and het-d genes.",

Espagn. AP223582; AAL372981; -.

EMBL, AP223582; AAL372981; -.

EMBL, AP223582; AAL372981; -.

InterPro; IPR001181; NACHT_NTPase.

InterPro; IPR001681; WD40.

Pfam; PF00400; WD40; 10.

PRINTS; PR00320; GPROTEINBRPT.
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Local Similarity 27.9%; Pred. No. 9e-25;
nes 129; Conservative 78; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1356 AA; 149720 MW; 9A80777304B361D0 CRC64;
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232
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                                                                                                                                                                                                                                                                                                                                                                                           78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAATNQQGSAKNGE-----NT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ANGEENGAHTIANNHIDMMEV----DGD-VEIPSNKAVV------LRGHESEV 172
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      173 FICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 ANLMIASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                               DB 3; Length 1356;
                                                                                                                                                                                                                                                                                                                            Query Match 17.3%; Score 472; DB 3; Length 13: Best Local Similarity 27.7%; Pred. No. 2e-24; Matches 128; Conservative 78; Mismatches 194; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 TOTGALVHSYRGTGG-IFEVCWNAAGDKVGASASDGSVCVLD 511
SEQUENCE FROM N.A.
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